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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:01:47 ; Search time 147.75 Seconds
(without alignments)
1287.197 Million cell updates/sec

Title: US-10-693-367-2

Perfect score: 3090

Sequence: 1 MFGKKRKRVEISAPSNFHR.....LAKAGPPASIVPLMRQNRTR 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3090	100.0	591	10	US-09-291-417-103
2	3090	100.0	591	14	US-10-134-102-4
3	3090	100.0	591	15	US-10-394-322A-48
4	3090	100.0	591	16	US-10-693-367-2
5	3075	99.5	588	14	US-10-134-102-1
6	2073	67.1	398	10	US-09-291-417-30
7	1748	56.6	719	14	US-10-331-095-2
8	1731	56.0	719	14	US-10-331-095-4
9	1731	56.0	719	15	US-10-394-322A-49
10	1502	48.6	292	15	US-10-406-676-5
11	1502	48.6	292	15	US-10-406-676-6
12	1502	48.6	292	15	US-10-406-676-8
13	1502	48.6	292	15	US-10-406-676-9
14	1502	48.6	292	15	US-10-406-676-10
15	1502	48.6	292	15	US-10-406-676-11

16	1502	48.6	293	15	US-10-406-676-4	Sequence 4, Appli
17	1497.5	48.5	639	14	US-10-134-102-6	Sequence 6, Appli
18	1494.5	48.4	635	14	US-10-134-102-2	Sequence 2, Appli
19	1481	47.9	292	15	US-10-406-676-7	Sequence 7, Appli
20	1481	47.9	292	15	US-10-406-676-12	Sequence 12, Appli
21	1473.5	47.7	681	10	US-09-291-417-29	Sequence 29, Appli
22	1470.5	47.6	681	10	US-09-765-815-2	Sequence 2, Appli
23	1421	46.0	292	15	US-10-406-676-15	Sequence 15, Appli
24	1335.5	43.2	641	16	US-10-311-034-15	Sequence 13, Appli
25	1303	42.2	290	15	US-10-406-676-13	Sequence 14, Appli
26	1289	41.7	290	15	US-10-406-676-14	Sequence 16, Appli
27	1289	41.7	290	15	US-10-406-676-16	Sequence 17, Appli
28	1289	41.7	290	15	US-10-406-676-17	Sequence 3, Appli
29	1277	41.3	250	16	US-10-693-367-3	Sequence 18, Appli
30	1213	39.3	290	15	US-10-406-676-18	Sequence 19, Appli
31	1209	39.1	290	15	US-10-406-676-20	Sequence 20, Appli
32	1209	39.1	290	15	US-10-406-676-21	Sequence 21, Appli
33	1147	37.1	292	15	US-10-406-676-21	Sequence 6482, Ap
34	1096.5	35.5	540	15	US-10-369-493-6482	Sequence 6483, Ap
35	1090.5	35.3	542	15	US-10-108-260A-3288	Sequence 3288, App
36	1024.5	33.2	580	15	US-10-267-502-378	Sequence 382, App
37	937.5	30.3	704	12	US-10-267-502-382	Sequence 6, Appli
38	924	29.9	544	12	US-09-967-624-6	Sequence 379, App
39	909	29.4	544	12	US-10-267-502-379	Sequence 6, Appli
40	909	29.4	544	14	US-10-289-161A-6	Sequence 47, Appli
41	909	29.4	544	15	US-10-394-322A-47	Sequence 95, Appli
42	909	29.4	544	10	US-09-291-417-95	Sequence 749, App
43	907	29.4	544	10	US-10-072-012-749	Sequence 4, Appli
44	904	29.3	524	12	US-10-029-905-4	
45	904	29.3	524	13		

ALIGNMENTS

RESULT 1

US-09-291-417-103
; Sequence 103, Application US/09291417A
; Publication No. US20030050230A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 240/300
; CURRENT APPLICATION NUMBER: US/09/291,417A
; CURRENT FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: US 60/081,784
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 103
; TYPE: PRT
; ORGANISM: Full Length Mammalian (Human) PAK5hu
US-09-291-417-103

Query Match 100.0%; Score 3090; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.4e-167;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MFGKKRKRVEISAPSNFHRVHTGFDQHQKFTGLPRQWSLIEESARRPKPLVDPA	60
DB	1	MFGKKRKRVEISAPSNFHRVHTGFDQHQKFTGLPRQWSLIEESARRPKPLVDPA	60
QY	61	SIQGPAPKTIYRSGKAGKOGALTLLDEFENWSTRTNSLRDPPPPARARQENGMEE	120
DB	61	SIQGPAPKTIYRSGKAGKOGALTLLDEFENWSTRTNSLRDPPPPARARQENGMEE	120
QY	121	PATTARGGPGKAGRGREFAGHSEAGGSGDRRRAGPEKRRPKSSREGSGGPQESSRDKRPL	180
DB	121	PATTARGGPGKAGRGREFAGHSEAGGSGDRRRAGPEKRRPKSSREGSGGPQESSRDKRPL	180

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QY 181 SGPVGTGPAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEHDPVAPNGSPSAGGLAIP 240
Db 181 SGPVGTGPAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEHDPVAPNGSPSAGGLAIP 240
QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPPSPQREPQVRS 300
Db 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPPSPQREPQVRS 300
QY 301 HEGFRAALQVVDGPPRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQORR 360
Db 301 HEGFRAALQVVDGPPRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQORR 360
QY 361 ELLFNEVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGALTDIVTHRMNEEQIAAV 420
Db 361 ELLFNEVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGALTDIVTHRMNEEQIAAV 420
QY 421 CLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTTPY 480
Db 421 CLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTTPY 480
QY 481 WNAPELISRLPYGPEVDIWSLGIWVEMVDGPPYFNEPPLKAMKMIKMDLPPRLKNLHK 540
Db 481 WNAPELISRLPYGPEVDIWSLGIWVEMVDGPPYFNEPPLKAMKMIKMDLPPRLKNLHK 540
QY 541 VSPSLKGFLLRDLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMQNRTR 591
Db 541 VSPSLKGFLLRDLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMQNRTR 591

RESULT 2
US-10-134-102-4
; Sequence 4, Application US/10134102
; Publication No. US20030186254A1
; GENERAL INFORMATION:
; APPLICANT: Melnick, Michael B.
; APPLICANT: Moritz, Albrecht
; APPLICANT: Comb, Michael J.
; TITLE OF INVENTION: Regulation of HIV-Tat and Nef by the Pak4 kinase and its
; FILE REFERENCE: CST-176 CIP
; CURRENT APPLICATION NUMBER: US/10/134,102
; CURRENT FILING DATE: 2002-04-29
; PRIOR FILING DATE: 09/750,457
; PRIOR FILING DATE: 2000-12-28
; PRIOR FILING DATE: 60/173,939
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-134-102-4

Query Match 100.0%; Score 3090; DB 14; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.4e-167;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGKRRKRVETISAPSNFEHRVHTGFDQHEQKFTGLPRQWSLIEESARRPKPLVDPAICIT 60
Db 1 MFGKRRKRVETISAPSNFEHRVHTGFDQHEQKFTGLPRQWSLIEESARRPKPLVDPAICIT 60
QY 61 SIOPGAPKTIVRSGKAGKAGLTLILLDEFENMSVTRNSLRDSSPPPPARQNGMPPEE 120
Db 61 SIOPGAPKTIVRSGKAGKAGLTLILLDEFENMSVTRNSLRDSSPPPPARQNGMPPEE 120
QY 121 PATTARGGPGKAGSRGFRAGHSEAGGSGGRRRAGPEKPKSSREGSGGQESRDKRPL 180
Db 121 PATTARGGPGKAGSRGFRAGHSEAGGSGGRRRAGPEKPKSSREGSGGQESRDKRPL 180
QY 181 SGPVGTGPAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEHDPVAPNGSPSAGGLAIP 240
Db 181 SGPVGTGPAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEHDPVAPNGSPSAGGLAIP 240
QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPPSPQREPQVRS 300
Db 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPPSPQREPQVRS 300
QY 301 HEGFRAALQVVDGPPRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQORR 360
Db 301 HEGFRAALQVVDGPPRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQORR 360
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QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPPSPQREPQVRS 300
Db 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPPSPQREPQVRS 300
QY 301 HEGFRAALQVVDGPPRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQORR 360
Db 301 HEGFRAALQVVDGPPRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQORR 360
QY 361 ELLFNEVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGALTDIVTHRMNEEQIAAV 420
Db 361 ELLFNEVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGALTDIVTHRMNEEQIAAV 420
QY 421 CLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTTPY 480
Db 421 CLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTTPY 480
QY 481 WNAPELISRLPYGPEVDIWSLGIWVEMVDGPPYFNEPPLKAMKMIKMDLPPRLKNLHK 540
Db 481 WNAPELISRLPYGPEVDIWSLGIWVEMVDGPPYFNEPPLKAMKMIKMDLPPRLKNLHK 540
QY 541 VSPSLKGFLLRDLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMQNRTR 591
Db 541 VSPSLKGFLLRDLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMQNRTR 591

RESULT 3
US-10-394-322A-48
; Sequence 48, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-48

Query Match 100.0%; Score 3090; DB 15; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.4e-167;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGKRRKRVETISAPSNFEHRVHTGFDQHEQKFTGLPRQWSLIEESARRPKPLVDPAICIT 60
Db 1 MFGKRRKRVETISAPSNFEHRVHTGFDQHEQKFTGLPRQWSLIEESARRPKPLVDPAICIT 60
QY 61 SIOPGAPKTIVRSGKAGKAGLTLILLDEFENMSVTRNSLRDSSPPPPARQNGMPPEE 120
Db 61 SIOPGAPKTIVRSGKAGKAGLTLILLDEFENMSVTRNSLRDSSPPPPARQNGMPPEE 120
QY 121 PATTARGGPGKAGSRGFRAGHSEAGGSGGRRRAGPEKPKSSREGSGGQESRDKRPL 180
Db 121 PATTARGGPGKAGSRGFRAGHSEAGGSGGRRRAGPEKPKSSREGSGGQESRDKRPL 180
QY 181 SGPVGTGPAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEHDPVAPNGSPSAGGLAIP 240
Db 181 SGPVGTGPAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEHDPVAPNGSPSAGGLAIP 240
QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPPSPQREPQVRS 300
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QY 301 HEGFRAALQVVDGPPRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQORR 360
Db 301 HEGFRAALQVVDGPPRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQORR 360
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301 HEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSKGLVAVKMDLRKQRR 360
361 ELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEQIAAV 420
361 ELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEQIAAV 420
421 CLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPT 480
421 CLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPT 480
481 WMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYFNEPPLKAMKIMRDNLPPRLKNLHK 540
481 WMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYFNEPPLKAMKIMRDNLPPRLKNLHK 540
541 VSPSLKGFLLRDLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
541 VSPSLKGFLLRDLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

RESULT 4
US-10-693-367-2
; Sequence 2, Application US/10693367
; Publication No. US2004009192A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
; FILE REFERENCE: 575/55311-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/693,367
; CURRENT FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: US/09/718,032
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11341
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/082,737
; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 591
; TYPE: PRT
; ORGANISM: human
US-10-693-367-2

Query Match 100.0%; Score 3090; DB 16; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.4e-167;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGKRRKVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIEESARRPKPLVDPACIT 60
DB 1 MFGKRRKVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIEESARRPKPLVDPACIT 60
QY 61 SIOPGAPKTIVRGSKGADGALTLLDDEFENMVSRTNSLRDSDPPPPARARQENGMPPEE 120
DB 61 SIOPGAPKTIVRGSKGADGALTLLDDEFENMVSRTNSLRDSDPPPPARARQENGMPPEE 120
QY 61 SIOPGAPKTIVRGSKGADGALTLLDDEFENMVSRTNSLRDSDPPPPARARQENGMPPEE 120
DB 61 SIOPGAPKTIVRGSKGADGALTLLDDEFENMVSRTNSLRDSDPPPPARARQENGMPPEE 120
QY 121 PATTARGGPGKAGSRGFAGHSEAGGSGDRRRAGPEKPKSRREGSGGPPQESSRDKRPL 180
DB 121 PATTARGGPGKAGSRGFAGHSEAGGSGDRRRAGPEKPKSRREGSGGPPQESSRDKRPL 180
QY 181 SGPDVGTTPQAGLASGAKLAAGRPNFTYPRADTDHPSRGAQGEHVDVAPNGPSAGGLAIP 240
DB 181 SGPDVGTTPQAGLASGAKLAAGRPNFTYPRADTDHPSRGAQGEHVDVAPNGPSAGGLAIP 240
QY 181 SGPDVGTTPQAGLASGAKLAAGRPNFTYPRADTDHPSRGAQGEHVDVAPNGPSAGGLAIP 240
DB 181 SGPDVGTTPQAGLASGAKLAAGRPNFTYPRADTDHPSRGAQGEHVDVAPNGPSAGGLAIP 240
QY 241 QSSSSSRPPPTTRARGAPSPGVLGPHASEPQLAPACTPAAPVAPGPPGPRSPQREPQVRS 300
DB 241 QSSSSSRPPPTTRARGAPSPGVLGPHASEPQLAPACTPAAPVAPGPPGPRSPQREPQVRS 300
QY 301 HEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSKGLVAVKMDLRKQRR 360
DB 301 HEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSKGLVAVKMDLRKQRR 360
QY 361 ELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEQIAAV 420
DB 361 ELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEQIAAV 420

361 ELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEQIAAV 420
421 CLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPT 480
421 CLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPT 480
481 WMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYFNEPPLKAMKIMRDNLPPRLKNLHK 540
481 WMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYFNEPPLKAMKIMRDNLPPRLKNLHK 540
541 VSPSLKGFLLRDLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
541 VSPSLKGFLLRDLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

RESULT 5
US-10-134-102-1
; Sequence 1, Application US/10134102
; Publication No. US20030186254A1
; GENERAL INFORMATION:
; APPLICANT: Moritz, Michael B.
; APPLICANT: Comb, Michael J.
; TITLE OF INVENTION: Regulation of HIV-Tat and Nef by the Pak4 kinase and its
; TITLE OF INVENTION: binding partners and methods of identifying modulators thereof.
; FILE REFERENCE: CST-176 CIP
; CURRENT APPLICATION NUMBER: US/10/134,102
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 09/750,457
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/173,939
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-134-102-1

Query Match 99.5%; Score 3075; DB 14; Length 588;
Best Local Similarity 100.0%; Pred. No. 9.8e-167;
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGKRRKVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIEESARRPKPLVDPACIT 60
DB 1 MFGKRRKVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIEESARRPKPLVDPACIT 60
QY 61 SIOPGAPKTIVRGSKGADGALTLLDDEFENMVSRTNSLRDSDPPPPARARQENGMPPEE 120
DB 61 SIOPGAPKTIVRGSKGADGALTLLDDEFENMVSRTNSLRDSDPPPPARARQENGMPPEE 120
QY 121 PATTARGGPGKAGSRGFAGHSEAGGSGDRRRAGPEKPKSRREGSGGPPQESSRDKRPL 180
DB 121 PATTARGGPGKAGSRGFAGHSEAGGSGDRRRAGPEKPKSRREGSGGPPQESSRDKRPL 180
QY 181 SGPDVGTTPQAGLASGAKLAAGRPNFTYPRADTDHPSRGAQGEHVDVAPNGPSAGGLAIP 240
DB 181 SGPDVGTTPQAGLASGAKLAAGRPNFTYPRADTDHPSRGAQGEHVDVAPNGPSAGGLAIP 240
QY 241 QSSSSSRPPPTTRARGAPSPGVLGPHASEPQLAPACTPAAPVAPGPPGPRSPQREPQVRS 300
DB 241 QSSSSSRPPPTTRARGAPSPGVLGPHASEPQLAPACTPAAPVAPGPPGPRSPQREPQVRS 300
QY 301 HEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSKGLVAVKMDLRKQRR 360
DB 301 HEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSKGLVAVKMDLRKQRR 360
QY 361 ELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEQIAAV 420
DB 361 ELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEQIAAV 420

QY 421 CLAVLQALSVLHAQVTHRDIKSDSIILLTHDGRVKLSDFGFCQAVSKEVPRKSLVGTPY 480
Db 421 CLAVLQALSVLHAQVTHRDIKSDSIILLTHDGRVKLSDFGFCQAVSKEVPRKSLVGTPY 480
QY 481 WMAPELISRLPYGPEVDIWSLGINVIMVWDEGPEPPYFNEPPLKAMKMRDNLPPRLKNLHK 540
Db 481 WMAPELISRLPYGPEVDIWSLGINVIMVWDEGPEPPYFNEPPLKAMKMRDNLPPRLKNLHK 540
QY 541 VSPSLKGFDRLLVRDPAQATRAEALLKHPFLAKAGPPASIVPLMRQN 588
Db 541 VSPSLKGFDRLLVRDPAQATRAEALLKHPFLAKAGPPASIVPLMRQN 588

RESULT 6

US-09-291-417-30
; Sequence 30, Application US/09291417A
; Publication No. US20030050230A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 240/300
; CURRENT APPLICATION NUMBER: US/09/291,417A
; EARLIER FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: US 60/081,784
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Mammalian (Human) PAK5
US-09-291-417-30

Query Match 67.1%; Score 2073; DB 10; Length 398;
Best Local Similarity 100.0%; Pred. No. 5,3e-110;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 ASGAKLAAGRPTNTYPRADTDHPSRGAQGEHDVAPNGSPSAGGLAIPOSSSSSRPPTRA 253
Db 1 ASGAKLAAGRPTNTYPRADTDHPSRGAQGEHDVAPNGSPSAGGLAIPOSSSSSRPPTRA 60
QY 254 RGAPSPGVLGPHASBPQAPACTPAAPVPGPRSPQRPQVSHQFRAALQLVVD 313
Db 61 RGAPSPGVLGPHASBPQAPACTPAAPVPGPRSPQRPQVSHQFRAALQLVVD 120
QY 314 PGDPRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVIMRDY 373
Db 121 PGDPRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVIMRDY 180
QY 374 QHENVVMYNSLYVGDELWVWMEFLEGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHA 433
Db 181 QHENVVMYNSLYVGDELWVWMEFLEGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHA 240
QY 434 QGVTHRDIKSDSIILLTHDGRVKLSDFGFCQAVSKEVPRKSLVGTPYFNEPPLKAMKMRDNLPPRLKNLHK 493
Db 241 QGVTHRDIKSDSIILLTHDGRVKLSDFGFCQAVSKEVPRKSLVGTPYFNEPPLKAMKMRDNLPPRLKNLHK 300
QY 494 PEVDIWSLGINVIMVWDEGPEPPYFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFDRLL 553
Db 301 PEVDIWSLGINVIMVWDEGPEPPYFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFDRLL 360
QY 554 VRDPAQATRAEALLKHPFLAKAGPPASIVPLMRQNRT 591
Db 361 VRDPAQATRAEALLKHPFLAKAGPPASIVPLMRQNRT 398

RESULT 7

US-10-331-095-2
; Sequence 2, Application US/10331095
; Publication No. US20030124107A1
; GENERAL INFORMATION:

; APPLICANT: Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK5-Related Compositions and Methods
; FILE REFERENCE: 0575/64083-A
; CURRENT APPLICATION NUMBER: US/10/331,095
; CURRENT FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: 60/343,972
; PRIOR FILING DATE: 2001-12-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: mouse PAK5
US-10-331-095-2

Query Match 56.6%; Score 1748; DB 14; Length 719;
Best Local Similarity 52.9%; Pred. No. 2.9e-91;
Matches 385; Conservative 65; Mismatches 128; Indels 150; Gaps 16;
QY 1 MFGKRRKRVETISAPSNFEHRVHTGPDQHEQKFTGLPRQWOSLIEESARRPKPLVDACIT 60
Db 1 MFGKRRKRVETISAPSNFEHRVHTGPDQHEQKFTGLPRQWOSLIEESARRPKPLVDACIT 60
QY 61 STOPGAPKTIIVRGSGAKGALTLTLLDEPENSVTRNSLRDRSPPPP---ARAR----- 112
Db 61 PIQLAPMKTIIVRGSKSCKTSINLLEDFDNIISVTRNSLRKESPTTPQGAASRIQGH 120
QY 113 QENGM-----PEEPATTARGGPGKAGSGRA-----CH----- 141
Db 121 EENGFTTSQYSSSESDTTADYITEKYRDRSLRGDDLDLYKSSHAQKQNGHAKMKHGDA 180
QY 142 -----SEAGGSGDRRA----- 154
Db 181 YYPEMKSLKTLDLAGFPVDVHTHLSLRKSSEYGLDRWDYQRASSSSPLDYSFLTSPRTA 240
QY 155 -----GP-----EKRPKSREGSGGQESRDRKPLSGPDVGTTP-QPA 191
Db 241 GTSRCSKESLAYSESDWGPGLDDYDRRPKSSYLHOTSQPAMR-ORSKSGSLQEPMMFP 299
QY 192 GLASGAKLAAGRPTNTY-----BRADTTH-----PSRGAQGEHDVAPNGP 232
Db 300 GASAFKTHPQCHSYNSYTYPRLSEPTMCIKVDYDRAQWVFPSPPLSGS-----DTPYRGP 354
QY 233 SAGGLAIPOS-----SSSSSRPPTRARGA-----PSGVLGPHASEPQLAPPACTPAAP 281
Db 355 T---KLPQSQSKAGYSSGSHQYFSGYHKASLYHHPSLQTSQYISTASYL-SSLISSS 409
QY 282 AVPGPPGPRSPQRPQVSHQFRAALQLVVDGDPRLSYLDNFIKIGEGSTGIVCIATVR 341
Db 410 TYPSPSSGSSDQGFQVSHQFRAALQLVVDGDPRLSYLDNFIKIGEGSTGIVCIATEK 469
QY 342 SSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVMYNSLYVGDELWVWMEFLEGG 401
Db 470 HTGQVAVKMDLRKQORRELLFNEVIMRDYHNDVVDVMSYLVGDELWVWMEFLEGG 529
QY 402 ALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVTHRDIKSDSIILLTHDGRVKLSDFG 461
Db 530 ALTDIVTHTRMNEEQIAATVCLSVLKALSYLHNQGVTHRDIKSDSIILLTHDGRVKLSDFG 589
QY 462 CAQVSKEVPRKSLVGTPYFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFDRLL 521
Db 590 CAQVSKEVPRKSLVGTPYFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFDRLL 649
QY 522 KAMKMRDNLPPRLKNLHKVSPSLKGFDRLLVRDPAQATRAEALLKHPFLAKAGPPASI 581
Db 650 QAMRIRDSLPVRKDLHKVSMRLRGFLDMLVREPSQRATAQELLGHPPFLKAGPPSCI 709
QY 582 VPLMRQN 589
|||||

Db 710 VPLMRQYR 717

RESULT 8

US-10-331-095-4

; Sequence 4, Application US/10331095

; Publication No. US20030124107A1

; GENERAL INFORMATION:

; APPLICANT: Columbia University

; APPLICANT: Minden, Audrey

; TITLE OF INVENTION: PAKS-Related Compositions and Methods

; FILE REFERENCE: 0575/64083-A

; CURRENT APPLICATION NUMBER: US/10/331,095

; CURRENT FILING DATE: 2002-12-27

; PRIOR APPLICATION NUMBER: 60/343,972

; PRIOR FILING DATE: 2001-12-28

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 719

; TYPE: PRT

; ORGANISM: human

; FEATURE:

; NAME/KEY: MISC_FEATURE

; OTHER INFORMATION: Human PAKS

US-10-331-095-4

Query Match 56.0%; Score 1731; DB 14; Length 719;

Best Local Similarity 52.4%; Pred. No. 2.6e-90;

Matches 383; Conservative 66; Mismatches 126; Indels 156; Gaps 17;

QY 1 MFGKRRKRVVEISAPNFEHRVHTGPDQHQKFTGLPRQWSLIEESARRPKPLVDPACT 60

Db 1 MFGKRRKRVVEISAPNFEHRVHTGPDQHQKFTGLPRQWSLIEESARRPKPLVDPACT 60

QY 61 SIOPGAKTIVRGSKAKGALTLLEDEFENSVTRSNLRRDSDPPPPARA-----R 112

Db 61 SIOPGAKTIVRGSKAKGALTLLEDEFENSVTRSNLRRDSDPPPPARA-----R 112

QY 113 QENGM-----PREPATT-----RG-----PGKA 132

Db 113 QENGM-----PREPATT-----RG-----PGKA 132

QY 121 EENGFTIFSQYSESDDTADYTKYREKSLYGDLDPPYVRGSHAAKQNGHVMKMGHEA 180

Db 121 EENGFTIFSQYSESDDTADYTKYREKSLYGDLDPPYVRGSHAAKQNGHVMKMGHEA 180

QY 133 -----GSRGRFAGH-----SEAG 145

Db 133 -----GSRGRFAGH-----SEAG 145

QY 181 YYSEVKPLKSDFAFADYHSHLDSLKPSEYSDLKWEYORASSSSPLDYSFQFTPRTA 240

Db 181 YYSEVKPLKSDFAFADYHSHLDSLKPSEYSDLKWEYORASSSSPLDYSFQFTPRTA 240

QY 146 GSGDRRRA-----GP-----EKRPKSSREGSGGPOESSRDKRPLSGPDVGTGTP-QPA 191

Db 146 GSGDRRRA-----GP-----EKRPKSSREGSGGPOESSRDKRPLSGPDVGTGTP-QPA 191

QY 241 GTSGCKESLAYSESEWGPSLDDYDRPKSYLNOTSPQPTMR-QRSRSGSLQEPMPWF 299

Db 241 GTSGCKESLAYSESEWGPSLDDYDRPKSYLNOTSPQPTMR-QRSRSGSLQEPMPWF 299

QY 192 GLASGAKLAAGRPNNTY-----PRADTDH-----PSRGAQGEPHDVAENG 232

Db 192 GLASGAKLAAGRPNNTY-----PRADTDH-----PSRGAQGEPHDVAENG 232

QY 300 GASAFKTHPQHSYNSYTPRLSEPTWCIPKVDYDRAQMVLSPPPLSGS-----DTYPRGP 354

Db 300 GASAFKTHPQHSYNSYTPRLSEPTWCIPKVDYDRAQMVLSPPPLSGS-----DTYPRGP 354

QY 233 SAGGLAIPOS-----SSSSSRPPTARGAPSPGVLPFHASEPOLAPACTP----- 278

Db 233 SAGGLAIPOS-----SSSSSRPPTARGAPSPGVLPFHASEPOLAPACTP----- 278

QY 355 A-----KLPSQSKSGYSSSHQPSGYHKA-----TLYHHPFSLOQSSQVISTASYLSLSL 406

Db 355 A-----KLPSQSKSGYSSSHQPSGYHKA-----TLYHHPFSLOQSSQVISTASYLSLSL 406

QY 279 AAPAVPGPPGPRSPQREPVSHQFRAALQVVDGPDPRSYLDFNFIKIGSGSTGIVCIA 338

Db 279 AAPAVPGPPGPRSPQREPVSHQFRAALQVVDGPDPRSYLDFNFIKIGSGSTGIVCIA 338

QY 407 SSSTYPSPSGSSDQPPSRVSHQFRAALQVVDGPDPRSYLDFNFIKIGSGSTGIVCIA 466

Db 407 SSSTYPSPSGSSDQPPSRVSHQFRAALQVVDGPDPRSYLDFNFIKIGSGSTGIVCIA 466

QY 339 TVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMNSYLVGLDELVWMEFL 398

Db 339 TVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMNSYLVGLDELVWMEFL 398

QY 467 TEKHTGKQVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMNSYLVGLDELVWMEFL 526

Db 467 TEKHTGKQVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMNSYLVGLDELVWMEFL 526

QY 399 EGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD 458

Db 399 EGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD 458

QY 527 EGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD 586

Db 527 EGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD 586

QY 459 PGCAQVSKVEPKKSLVGTPTWMAPEVIRLPGYGTVDVNSLGIWMIEMIDGPPYPNE 518

Db 459 PGCAQVSKVEPKKSLVGTPTWMAPEVIRLPGYGTVDVNSLGIWMIEMIDGPPYPNE 518

Db 710 VPLMRQYR 717

RESULT 8

US-10-331-095-4

; Sequence 4, Application US/10331095

; Publication No. US20030124107A1

; GENERAL INFORMATION:

; APPLICANT: Columbia University

; APPLICANT: Minden, Audrey

; TITLE OF INVENTION: PAKS-Related Compositions and Methods

; FILE REFERENCE: 0575/64083-A

; CURRENT APPLICATION NUMBER: US/10/331,095

; CURRENT FILING DATE: 2002-12-27

; PRIOR APPLICATION NUMBER: 60/343,972

; PRIOR FILING DATE: 2001-12-28

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 719

; TYPE: PRT

; ORGANISM: human

; FEATURE:

; NAME/KEY: MISC_FEATURE

; OTHER INFORMATION: Human PAKS

US-10-331-095-4

Query Match 56.0%; Score 1731; DB 14; Length 719;

Best Local Similarity 52.4%; Pred. No. 2.6e-90;

Matches 383; Conservative 66; Mismatches 126; Indels 156; Gaps 17;

QY 1 MFGKRRKRVVEISAPNFEHRVHTGPDQHQKFTGLPRQWSLIEESARRPKPLVDPACT 60

Db 1 MFGKRRKRVVEISAPNFEHRVHTGPDQHQKFTGLPRQWSLIEESARRPKPLVDPACT 60

QY 61 SIOPGAKTIVRGSKAKGALTLLEDEFENSVTRSNLRRDSDPPPPARA-----R 112

Db 61 SIOPGAKTIVRGSKAKGALTLLEDEFENSVTRSNLRRDSDPPPPARA-----R 112

QY 113 QENGM-----PREPATT-----RG-----PGKA 132

Db 113 QENGM-----PREPATT-----RG-----PGKA 132

QY 121 EENGFTIFSQYSESDDTADYTKYREKSLYGDLDPPYVRGSHAAKQNGHVMKMGHEA 180

Db 121 EENGFTIFSQYSESDDTADYTKYREKSLYGDLDPPYVRGSHAAKQNGHVMKMGHEA 180

QY 133 -----GSRGRFAGH-----SEAG 145

Db 133 -----GSRGRFAGH-----SEAG 145

QY 181 YYSEVKPLKSDFAFADYHSHLDSLKPSEYSDLKWEYORASSSSPLDYSFQFTPRTA 240

Db 181 YYSEVKPLKSDFAFADYHSHLDSLKPSEYSDLKWEYORASSSSPLDYSFQFTPRTA 240

QY 146 GSGDRRRA-----GP-----EKRPKSSREGSGGPOESSRDKRPLSGPDVGTGTP-QPA 191

Db 146 GSGDRRRA-----GP-----EKRPKSSREGSGGPOESSRDKRPLSGPDVGTGTP-QPA 191

QY 241 GTSGCKESLAYSESEWGPSLDDYDRPKSYLNOTSPQPTMR-QRSRSGSLQEPMPWF 299

Db 241 GTSGCKESLAYSESEWGPSLDDYDRPKSYLNOTSPQPTMR-QRSRSGSLQEPMPWF 299

QY 192 GLASGAKLAAGRPNNTY-----PRADTDH-----PSRGAQGEPHDVAENG 232

Db 192 GLASGAKLAAGRPNNTY-----PRADTDH-----PSRGAQGEPHDVAENG 232

QY 300 GASAFKTHPQHSYNSYTPRLSEPTWCIPKVDYDRAQMVLSPPPLSGS-----DTYPRGP 354

Db 300 GASAFKTHPQHSYNSYTPRLSEPTWCIPKVDYDRAQMVLSPPPLSGS-----DTYPRGP 354

QY 233 SAGGLAIPOS-----SSSSSRPPTARGAPSPGVLPFHASEPOLAPACTP----- 278

Db 233 SAGGLAIPOS-----SSSSSRPPTARGAPSPGVLPFHASEPOLAPACTP----- 278

QY 355 A-----KLPSQSKSGYSSSHQPSGYHKA-----TLYHHPFSLOQSSQVISTASYLSLSL 406

Db 355 A-----KLPSQSKSGYSSSHQPSGYHKA-----TLYHHPFSLOQSSQVISTASYLSLSL 406

QY 279 AAPAVPGPPGPRSPQREPVSHQFRAALQVVDGPDPRSYLDFNFIKIGSGSTGIVCIA 338

Db 279 AAPAVPGPPGPRSPQREPVSHQFRAALQVVDGPDPRSYLDFNFIKIGSGSTGIVCIA 338

QY 407 SSSTYPSPSGSSDQPPSRVSHQFRAALQVVDGPDPRSYLDFNFIKIGSGSTGIVCIA 466

Db 407 SSSTYPSPSGSSDQPPSRVSHQFRAALQVVDGPDPRSYLDFNFIKIGSGSTGIVCIA 466

QY 339 TVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMNSYLVGLDELVWMEFL 398

Db 339 TVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMNSYLVGLDELVWMEFL 398

QY 467 TEKHTGKQVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMNSYLVGLDELVWMEFL 526

Db 467 TEKHTGKQVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMNSYLVGLDELVWMEFL 526

QY 399 EGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD 458

Db 399 EGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD 458

QY 527 EGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD 586

Db 527 EGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD 586

QY 459 PGCAQVSKVEPKKSLVGTPTWMAPEVIRLPGYGTVDVNSLGIWMIEMIDGPPYPNE 518

Db 459 PGCAQVSKVEPKKSLVGTPTWMAPEVIRLPGYGTVDVNSLGIWMIEMIDGPPYPNE 518

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Db 527 EGGALTDIVTHRMNEEQIATVLSVLRALSYLHQGVTHRDIKSDSILLTSDGRIKLSD 586
Qy 459 FGCAQVSKEVPRKSLVGTGYPMAPELISRLPYGPEVDIWSLGLIMVIMVDGPPYFNE 518
Db 587 FGCAQVSKEVPRKSLVGTGYPMAPELISRLPYGTEVDIWSLGLIMVIMVDGPPYFNE 646
Qy 519 PPLKAMKMIKMDNLPPLKKNLHKVSPSLKGFLLDRLVRDPAQATAAELLKHPFLAKAGPP 578
Db 647 PPLQAMRRIRDSLPVRVKDLHKVSSVLRGFLDMLVREPSORATAQELLGHFPLKAGPP 706
Qy 579 ASIVPLMRQNR 589
Db 707 SCIVPLMRQYR 717
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RESULT 10

US-10-406-676-5

; Sequence 5, Application US/10406676

; Publication No. US20030229453A1

; GENERAL INFORMATION:

; APPLICANT: Structural Genomix, Inc.

; APPLICANT: Antonyamy, Stephen

; APPLICANT: Feil, Ingeborg

; APPLICANT: Buchanan, Sean

; APPLICANT: Post, Kai W.

; APPLICANT: Liu, Yi

; APPLICANT: Lorber, David

; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE

; FILE OF INVENTION: PAK4KD

; FILE REFERENCE: 524982002300

; CURRENT APPLICATION NUMBER: US/10/406,676

; PRIOR FILING DATE: 2003-04-02

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/430,567

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 292

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-406-676-5

Query Match

Best Local Similarity 48.6%; Score 1502; DB 15; Length 292;

Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 300 SHEQFRAALQLVDPDPRSILDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQOR 359
Db 1 SHEQFRAALQLVDPDPRSILDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQOR 60
Qy 360 RELFNEVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGALTDIVTHRMNEEQIAA 419
Db 61 RELFNEVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGALTDIVTHRMNEEQIAA 120
Qy 420 VCLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGFCQVSKVPRKSLVGTG 479
Db 121 VCLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGFCQVSKVPRKSLVGTG 180
Qy 480 YWMAPELISRLPYGPEVDIWSLGLIMVIMVDGPPYFNEPPLKAMKMIKMDNLPPLK 539
Db 181 YWMAPELISRLPYGPEVDIWSLGLIMVIMVDGPPYFNEPPLKAMKMIKMDNLPPLK 240
Qy 540 KVSPSLKGFLLDRLVRDPAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
Db 241 KVSPSLKGFLLDRLVRDPAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 292
```

RESULT 11

US-10-406-676-6

; Sequence 6, Application US/10406676

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H.sapiens
US-10-406-676-8

Query Match      48.6%; Score 1502; DB 15; Length 292;
Best Local Similarity 100.0%; Pred. No. 1e-77;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 SHEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKKMDLRKQOR 359
DB 1 SHEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKKMDLRKQOR 60

QY 360 RELLEFNEVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGGALTDIVTHTRMNEEQIAA 419
DB 61 RELLEFNEVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGGALTDIVTHTRMNEEQIAA 120

QY 420 VCLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTP 479
DB 121 VCLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTP 180

QY 480 YWMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPFNEPPLKAMKMIKMDLPPRLKNLH 539
DB 181 YWMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPFNEPPLKAMKMIKMDLPPRLKNLH 240

QY 540 KVSFSLKGFLLRDLVDPQAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
DB 241 KVSFSLKGFLLRDLVDPQAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 292

RESULT 13
US-10-406-676-9
; Sequence 9, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonyasamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT FILING DATE: 2003-04-02
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H.sapiens
US-10-406-676-9

Query Match      48.6%; Score 1502; DB 15; Length 292;
Best Local Similarity 100.0%; Pred. No. 1e-77;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 SHEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKKMDLRKQOR 359
DB 1 SHEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKKMDLRKQOR 60

QY 360 RELLEFNEVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGGALTDIVTHTRMNEEQIAA 419
DB 61 RELLEFNEVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGGALTDIVTHTRMNEEQIAA 120

QY 420 VCLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTP 479
DB 121 VCLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTP 180

QY 480 YWMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPFNEPPLKAMKMIKMDLPPRLKNLH 539
DB 181 YWMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPFNEPPLKAMKMIKMDLPPRLKNLH 240

QY 540 KVSFSLKGFLLRDLVDPQAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
DB 241 KVSFSLKGFLLRDLVDPQAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 292

RESULT 14
US-10-406-676-10
; Sequence 10, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonyasamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT FILING DATE: 2003-04-02
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H.sapiens
US-10-406-676-10

Query Match      48.6%; Score 1502; DB 15; Length 292;
Best Local Similarity 100.0%; Pred. No. 1e-77;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 SHEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKKMDLRKQOR 359
DB 1 SHEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKKMDLRKQOR 60

QY 360 RELLEFNEVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGGALTDIVTHTRMNEEQIAA 419
DB 61 RELLEFNEVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGGALTDIVTHTRMNEEQIAA 120

QY 420 VCLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTP 479
DB 121 VCLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTP 180

QY 480 YWMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPFNEPPLKAMKMIKMDLPPRLKNLH 539
DB 181 YWMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPFNEPPLKAMKMIKMDLPPRLKNLH 240

QY 540 KVSFSLKGFLLRDLVDPQAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
DB 241 KVSFSLKGFLLRDLVDPQAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 292

RESULT 15
US-10-406-676-11
; Sequence 11, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
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; APPLICANT: Antonyamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4D KINASE
; FILE OF INVENTION: PAK4D
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H.sapiens
US-10-406-676-11

Query Match 48.6%; Score 1502; DB 15; Length 292;
Best Local Similarity 100.0%; Pred. No. 1e-77;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 300 SHEQFRAALQLVVDGDPSPSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKXMDLRKQOR 359
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 SHEQFRAALQLVVDGDPSPSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKXMDLRKQOR 60
QY 360 RELLENEVIMEDYOHENNVVENYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAA 419
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 RELLENEVIMEDYOHENNVVENYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAA 120
QY 420 VCLAVLQALSVLHAQGVHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRKSLVGTP 479
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 VCLAVLQALSVLHAQGVHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRKSLVGTP 180
QY 480 YWMAPELISRLPYGPEVDIWSLGINVIMVWDGEPYFNEPPLKAMKIRDNLPRLKNLH 539
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 YWMAPELISRLPYGPEVDIWSLGINVIMVWDGEPYFNEPPLKAMKIRDNLPRLKNLH 240
QY 540 KVSPLKGFLLRDLVRDPAQRATAELLKHPFLAKAGPPASTVPLMRQNRTR 591
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 KVSPLKGFLLRDLVRDPAQRATAELLKHPFLAKAGPPASTVPLMRQNRTR 292

Search completed: September 29, 2004, 18:09:25
Job time : 150.75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 17:57:52 ; Search time 43.4559 Seconds
(without alignments)
1308.205 Million cell updates/sec

Title: US-10-693-367-2
Perfect score: 3090
Sequence: 1 MFGKKKKVEISAPSNFEHR.....LAKAGPPASIVPLMRQNRTR 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- PIR 78:*
- 1: Pirl:*
- 2: Pirl2:*
- 3: Pirl3:*
- 4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1096.5	35.5	540	2 T19956	hypothetical prote
2	1090.5	35.3	542	2 T19952	hypothetical prote
3	917	29.7	544	2 A57597	beta-p21-activated
4	907	29.4	544	2 I49376	p21 activated kina
5	895.5	29.0	525	2 S58682	protein kinase, p2
6	892.5	28.9	545	2 G01973	p21-activated prot
7	892	28.9	544	2 S40482	serine/threonine-s
8	846.5	27.4	1230	2 T18256	probable serine/th
9	846.5	27.4	1230	2 T18259	serine/threonine p
10	837	27.1	939	2 S28394	probable serine/th
11	823.5	26.7	658	2 T39500	serine/threonine-s
12	814.5	26.4	658	2 S60170	protein kinase Pak
13	811.5	26.3	622	2 T15467	hypothetical prote
14	760	24.6	842	2 S60402	protein kinase CLA
15	722	23.4	378	2 T26684	hypothetical prote
16	697	22.6	589	2 T38086	serine/threonine-p
17	651.5	21.1	655	2 S51884	probable protein k
18	505	16.3	836	2 B96716	probable serine/th
19	498	16.1	471	2 T39232	probable serine th
20	494	16.0	1102	2 JC6316	probable serine k
21	478	15.5	653	2 T34356	hypothetical prote
22	476	15.4	819	2 A53714	protein kinase (BC
23	470.5	15.2	829	2 T29372	hypothetical prote
24	464	15.0	426	2 S71886	Ste20-like protein
25	463	15.0	1231	2 T18532	serine/threonine pr
26	462	15.0	1233	2 T14157	serine/threonine p
27	460	14.9	1206	2 T34021	protein kinase SK2
28	458.5	14.8	690	2 C96572	protein F12M16.4 [
29	455.5	14.7	1080	2 S48944	hypothetical prote

30 455 14.7 1233 2 T30989 serine/threonine p
31 450.5 14.6 312 2 T38525 serine/threonine p
32 445 14.4 1001 2 T17365 serine/threonine p
33 440.5 14.3 1075 2 T27623 hypothetical prote
34 440.5 14.3 1080 2 T27622 hypothetical prote
35 437.5 14.2 1062 2 S46367 protein kinase CDC
36 428 13.9 1228 2 T18897 hypothetical prote
37 424.5 13.7 659 1 A39723 protein kinase byr
38 421 13.6 553 2 T01479 hypothetical prote
39 419 13.6 883 2 A96662 hypothetical prote
40 417.5 13.5 1174 2 T43051 protein kinase C (

ALIGNMENTS

RESULT 1

T19956
hypothetical protein C45B11.1b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C:Accession: T19956
R:McMurray, A.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19202
A:Accession: T19956
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-540 <WIL>
A:Cross-references: EMBL:Z74029; PIDN:CAA98433.1; GSPDB:GN00023; CESP:C45B11.1b
A:Experimental source: clone C45B11
C:Genetics:
A:Gene: CESP:C45B11.1b
A:Map position: 5
A:Introns: 13/2; 62/3; 104/2; 231/3; 367/2; 469/3
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 35.5%; Score 1096.5; DB 2; Length 540;
Best Local Similarity 41.7%; Pred. No. 1.4e-31;
Matches 251; Conservative 67; Mismatches 151; Indels 133; Gaps 9;
QY 4 KRKRVEISAPSNFEHRVHTGPDHQKFTGLPRQWSLI--ESARRPKPLVDPACITS 61
Db 29 RKVKSEISTPSNFEHRIHAGFDARSCTYTGPKQWQALLGPPRSISRPKMVPDPSCITP 88
QY 62 IQPGAKTIVRGSGKAGKAGLTLLDDEFENMSTRNSLRDPPPPPARARQNGMPEEP 121
Db 89 VDVAELKTVIRGSSRYNSPLPGMTNSPMSVARNSLRISATASP----- 135
QY 122 ATTARGGCGKAGRGRFAGHSEAGGSGDGRRRRAGPEKRPKSSREGSGGPOESSRDKRPLS 181
Db 136 -----VVVSSARHSFRPTLPVVSQR----- 156
QY 182 GPDVGTQPAGLASGAKLAAGRPFNTYPRADTDHPSRGAGQGEHDVAPNGSPSAGGLAIPQ 241
Db 157 -----GYPF-----NDPSVAPLPL-- 170
QY 242 SSSSSRPPTFRAGAPSPGVLGP-----ASEPQLAPPACTEAPAPVPGPG 288
Db 171 ---RNQKPPM---STTFGVEKPHQOQIITIVAPSRITTPLOPKS-----PST 213
QY 289 PRSPQREP---QRVSHQEPRAALQLVVDPGDPSRYLDNFYIKIGEGSTGIVCIATVRSRGK 345
Db 214 PQAMRQPKCTEGVSDDEFRNALKFVVDGTDPRSDLTDYKQIGEGSTGVVAAAYKISTKQ 273
QY 346 LVAVKGMKDLRKQORRELLFNEVIMRDYQHENVVYMNSYLVGDELWVWMEFLEGGALTD 405
Db 274 IVAVKRMNLRKQORRELLFNEVSILOYQHPNIVRFFSSHLDVDELWVWMEFMEGGSLTD 333

QY 406 IVTHTRMNEQIAAACLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQV 465
Db 334 IVTATRTMTEPQIATISRQVLGALDFLHARKVTHRDIKSDSILLKRDGTVKLTDFGCGQL 393
QY 466 SKEVPRKSLVGTGYWMADELISRLPYGGEVDIWSLGIWVIEWVDGEPYFNFPPPLKAMK 525
Db 394 SEEVPRRLSLVGTGYWMAAEVIAREPYDTRADIWISFGIMLIEWVEGEPYFNFDPQFQAMK 453
QY 526 MIRDNLPPPLKNIHKVSPSLKGFLLRLVDRPAQRATAAELLKHPTFLAKAGPPASIVPLM 585
Db 454 RIRDEHEARFSRHAKVSVELSELLSHCIYKDNKRWPAKDLLRHPPFAKAQHSSTIAPLL 513
QY 586 RQ 587
Db 514 LQ 515

RESULT 2
T19952
hypothetical protein C45B11.1a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C:Accession: T19952
R:McMurray, A.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19202
A:Accession: T19952
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-542 <WIL>
A:Cross-references: EMBL:Z74029; PIDN:CAA98429.1; GSPDB:GN00023; CESP:C45B11.1a
A:Experimental source: clone C45B11
C:Genetics:
A:Gene: CESP:C45B11.1a
A:Map position: 5
A:Introns: 13/2; 62/3; 104/2; 233/3; 369/2; 470/3
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol

Query Match 35.3%; Score 1090.5; DB 2; Length 542;
Best Local Similarity 42.0%; Pred. No. 2.3e-31;
Matches 253; Conservative 69; Mismatches 149; Indels 131; Gaps 11;

QY 4 KKKKVEISAPNFEHRVHTGPDQHEQKFTGLPRQWQSLI--ESARRPKPLVDPACITS 61
Db 29 RKVKKEISTPSNFEHRIHAGFDARS GTYGLPKQWQALLGPPRSISRKPKWVDPSCITP 88
QY 62 IQPGAPKTIVRGSKGAKGALTLLLDEFENMVSRTSNLSLRDSDPPPPARQENGMPPEP 121
Db 89 VDVAELKTVIRP-----SSSPRYNSPLP-----FGMTNSP 119
QY 122 ATTARGPGKAGSRGRFAGHSEAGGSGDRRRAGPEKRPKPSREGSGGPQESSRDKRPLS 181
Db 120 MFSV---ARNSRLRISATASPVNVVSSARHSFRPTLPVSQR----- 158
QY 182 GPDVCTPQAGLASGAKLAAGRPNTYPRADTHPSRGAQGEPHDVAPNGPSAGGLAIPO 241
Db 159 -----GYFF-----NDPSYAPLPL-- 172
QY 242 SSSSSSRPPTRARGAPSPGVLGPH-----ASEPOLAPPACTPAAPAVPGPPG 288
Db 173 ---RNQKPEM---STTFGEVPEHQYQIITIVASRTTTPQLQPKS-----PST 215
QY 289 PRSPREP---QRVSHQFRAALQLVDPGDPSPRLDNFIKIGEGSTGIVCIATVRSRSGK 345
Db 216 PQAMRQPKCTEGVSDERFRLAKFVVDGTDPRSLTDYKQIGEGSTGVWEAAAYKISTKQ 275
QY 346 LVAVKKMDLRKQORRELLFNEVVIKRDYCHENVMYNSYLVDGLVWMEFLEGALTD 405
Db 276 IVAVKRNMLRKQORRELLFNEVSIILRQYQHPNIVRFFSHLVDDGLVWMEFMEGGSLTD 335
QY 406 IVTHTRMNEQIAAACLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQV 465

Db 336 IVTATRTMTEPQIATISRQVLGALDFLHARKVTHRDIKSDSILLKRDGTVKLTDFGCGQL 395
QY 466 SKEVPRKSLVGTGYWMADELISRLPYGGEVDIWSLGIWVIEWVDGEPYFNFPPPLKAMK 525
Db 396 SEEVPRRLSLVGTGYWMAAEVIAREPYDTRADIWISFGIMLIEWVEGEPYFNFDPQFQAMK 455
QY 526 MIRDNLPPPLKNIHKVSPSLKGFLLRLVDRPAQRATAAELLKHPTFLAKAGPPASIVPLM 585
Db 456 RIRDEHEARFSRHAKVSVELSELLSHCIYKDNKRWPAKDLLRHPPFAKAQHSSTIAPLL 515
QY 586 RQ 587
Db 516 LQ 517

RESULT 3
A57597
beta-p21-activated protein kinase - rat
N:Alternate names: beta-PAK
C:Species: Rattus norvegicus (Norway rat)
C>Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 24-Sep-1999
C:Accession: A57597
R:Wanser, E.; Chong, C.; Zhao, Z.S.; Leung, T.; Michael, G.; Hall, C.; Lim, L.
J. Biol. Chem. 270, 25070-25078, 1995
A:Title: Molecular cloning of a new member of the p21-Cdc42/Rac-activated kinase
A:Reference number: A57597; MUID:96027610; PMID:7559638
A:Accession: A57597
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-544 <MAN>
A:Cross-references: GB:U33314; NID:g1039424; PIDN:AAC52268.1; PID:g1039425
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
C:Keywords: ATP
F:266-519/Domain: protein kinase homology <KIN>
F:274-282/Region: protein kinase ATP-binding motif

Query Match 29.7%; Score 917; DB 2; Length 544;
Best Local Similarity 35.8%; Pred. No. 2.1e-25;
Matches 211; Conservative 87; Mismatches 165; Indels 126; Gaps 8;

QY 4 KKKKVEISAPNFEHRVHTGPDQHEQKFTGLPRQWQSLI-----ESARRPKPLVDP 56
Db 63 KEKERPEISLPSDFEHTIHVGFDVATGTEGTGIPQWARLLQTSNITKLEQKNPQAVLD- 121
QY 57 ACITSIQCAPKTIVRGSKGAKGALTLLLDEFENMVSRTSNLSLRDSDPPPPARQENG 116
Db 122 -----VLKPYDSKFTVNNQKYSFT----- 141
QY 117 MPEEPATTARGPGKAGSRGRFAGHSEAGGSGDRRRAGPEKRPKPSREGSGGPQESSRD 176
Db 142 -----SGDKSAHGVIAAHQ-----SNTKTASEPPLAPVSEDEEEDDEEDD 184
QY 177 KRPLSGPDVCTPQAGLASGAKLAAGRPNTYPRADTHPSRGAQGEPHDVAPNGPSAGG 236
Db 185 NEP---PPIVAPRPBHTKS-----IYTRSVVESIASPA-----APNKEATPP 223
QY 237 LAIPOSSSSRPPTRARGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGPPRSPREP 296
Db 224 SAENANSTLYNTRD-----QRRK 243
QY 297 QRVSHQFRAALQLVDPGDPSPRLDNFIKIGEGSTGIVCIATVRSRSGKLVAKKMDLRK 356
Db 244 SKMTDEETLEKLRISVSVGDEPKKYTRPEKIGQASGTVYALDITGOEVALKQNNLQ 303
QY 357 QORRELLFNEVVIKRDYCHENVMYNSYLVDGLVWMEFLEGALTDIVTHTRMNEQ 416
Db 304 QPKKELIINELVWRKNPNVNLDSILVGDGLVWVNEVLGAGSLTDVVTETCMDSGQ 363
QY 417 IAAVCLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVSPRKSIV 476
Db 364 IAAVCRECLQALDFLHSNQVTHRDIKSDNILLGMDGSKVLTDGFGCAQITPEQSRKSTW 423
QY 477 GTPYWMADELISRLPYGGEVDIWSLGIWVIEWVDGEPYFNFPPPLKAMKMDRLNLPPLK 536

RESULT 5

S58682

protein kinase, p21-activated (EC 2.7.1.1.-) - human

N/Alternate names: protein kinase PAK65; S6/H4 Kinase

C/Species: Homo sapiens (man)

C/Date: 22-Aug-1996 #sequence revision 06-Sep-1996 #text_change 24-Sep-1999

C/Accession: S58682; S55258; S55304; S58690; A57441

R/Sells, M.; Knause, U.J.; Bagrodia, S.; Ambrose, D.; Bokoch, G.M.; Chernoff, J.

submitted to the EMBL Data Library, April 1995

A/Description: Human p21-activated protein kinases regulate actin organization in mammalian cells

A/Reference number: S58682

A/Accession: S58682

A/Molecule type: DNA

A/Residues: 1-525 <SRL>

A/Cross-references: EMBL:U24153; NID:g780807; PIDN:AAA65442.1; PID:g780808

R/Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.

EMBO J. 14, 1970-1978, 1995

A/Title: A novel serine kinase activated by rac1/CDC42Hs-dependent autophosphorylation in cells

A/Reference number: S55258; MUID:95262637; PMID:7744004

A/Accession: S55258

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 'MEETQCKNLEL', 31-89, 'T', 91-149, 'F', 151-224, 'T', 226-328, 'R', 330-338, 340-525 <SRL>

A/Accession: S55304

A/Molecule type: protein

A/Residues: 402-418 <MAW>

R/Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.

EMBO J. 14, 4385, 1995

A/Reference number: S58690; MUID:96016211; PMID:7556080

A/Contents: erratum

A/Accession: S58690

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-30 <MAP>

R/Benner, G.E.; Dennis, P.B.; Masaracchia, R.A.

J. Biol. Chem. 270, 21121-21128, 1995

A/Title: Activation of an S6/H4 kinase (PAK 65) from human placenta by intramolecular and heteromultimeric interactions

A/Reference number: A57441; MUID:95403344; PMID:7673144

A/Accession: A57441

A/Molecule type: protein

A/Residues: 197-216; 402, 'S', 404-409 <BEN>

A/Experimental source: placenta

C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homologous to the p21-activated protein kinase

C/Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine kinase

F:247-501/Domain: protein kinase homology <KIN>

F:255-263/Region: protein kinase ATP-binding motif

F:197,402/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 29.0%; Score 895.5; DB 2; Length 525;
Best Local Similarity 34.9%; Pred. No. 1.1e-24;
Matches 211; Conservative 94; Mismatches 136; Indels 163; Gaps 14;

Qy 4 KRKKVEISAPSNFHRVHTGTQDQHQKFTGLPRQWSLIE-----ESARRPKPLVDP 56
Db 67 KEKEPEISPPSDFEHTIHVGFDVATGTEGMEQWALLQTSNITKLEKKKQAVLD- 125

Qy 57 ACITSIQGPAKTIVRGSKAKDGALTLLDEFENMVSRTSNLSRRD--SPPPPARAQE 114
Db 126 -----VLKFYD-----SNTVKQKLSFTPP-----EK 147

Qy 115 NCMPF-EPATTARGFGKAGSRPFAGHSEAGGSGDRRRAGPEKRPKSRGSGGPOES 173
Db 148 DGLPSGTPALNAKG-----TEA-----PAVTEEDDDEET 178

Qy 174 SRDKRPLSGFDVGTGPQAGLASGAKLAGRPFNTYPRADTHPSRGAQGEPHDVAPNGPS 233
Db 179 A-----PPVIAPRPDHTKS-----IYTRSVID-PVPAPVGDSh----- 210

Qy 234 AGGLAIPOSSSSRRPPTARGAPSPCVLGFHASEPQLAPPACTPAPAVDPGPRSPQ 293
Db 211 -----VDGAKSGLDKQ 221

QY	294	REPQRVSHEQ	PRAALQLVVD	PGDPRS	YLDNF	IKIGEG	STGI	VCIA	TVRS	SGKL	VAVKMD	353	
Db	222	KKKPM	TDDEE	IMEK	LRTT	ISG	DP	KKK	TV	YKIG	QG	ASGT	281
QY	354	LRKQ	RELL	ENF	VE	VM	RDY	O	HEN	V	VM	NS	412
Db	282	LQ	QPK	KE	L	I	NE	L	VM	K	NP	NI	341
QY	413	NEEQ	IA	AV	CL	AV	LQ	AL	SV	LH	AG	QV	472
Db	342	DEA	QIA	AV	CR	E	L	Q	A	E	L	H	401
QY	473	KSL	V	GT	P	Y	W	M	A	P	E	L	532
Db	402	STW	V	GT	P	Y	W	M	A	P	E	V	461
QY	533	PR	K	N	L	H	K	V	S	L	G	F	585
Db	462	PE	L	Q	N	P	K	E	L	S	I	F	521
QY	586	Q	R	N	R								
Db	522	K	S	N	R								

RESULT 6
G01773
p21-activated protein kinase - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999
C/Accession: G01773
R;Chernoff, J.
submitted to the EMBL Data Library, April 1995
A;Reference number: G08374
A;Accession: G01773
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-545 <CHE>
A;Cross-references: EMBL:U24152; NID:G780805; PIDN:AAA6S441.1; PID:G780806
C;Genetic:
A;Gene: Pak1
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
F;268-521/Domain: protein kinase homology <KIN>

Query Match	28.9%	Score	892.5	DB 2	Length	545			
Best Local Similarity	36.9%	Pred. No.	1.5e-24						
Matches	216	Conservative	82	Mismatches	166	Indels	121	Gaps	11
QY	4	KRKRVEISAPSFHEVHTGFCDOHEQKFTGLPQWQSLIEESARRPKPLVDPACITSIQ	63						
Db	68	KEXERTEISUPSFETHITHVGFDAVTEGFTQMEQWARLLQTSN	111						
QY	64	PGAPKTVIRSGKGAOKGALTLILDEFENMSTRNSLRDSDPPPPARARQENGMPPEEPAT	123						
Db	112	-----ITKSEQKNPQAVLDLVLEFYNSKKT-SNSQKYS-----	144						
QY	124	TARGGFKAGSGRRFPAGHSAGCGGSDRRRAGPEKRPKSSREGGQGESDRDKRPLSGP	183						
Db	145	-----FTDKSAEDYNSSNALNV-----KAVSETPAVPVSEDED-----	181						
QY	184	DVGTPOPGLAGSAGKLAAGRPENT-----YPRADTDHPSRGAGEHDVAPNGPFSAGGLAIP	240						
Db	182	DDATPPP-----VIAPEPHKSVYTSVI-----EPLVPTPT-----	214						
QY	241	QSSSSRRPPTRRAGAPSPGVLFPHASEPOLAPPACTPAAPAVPGPGRSPQREPQVRS	300						
Db	215	RDVATSPISPTENNTTP-----PDALTNT-----EKQKKKPKMS	249						
QY	301	HEQFRAALQLVDPDPSRLDNFIKIGEGSTGIVCIATVRSSGKLIVAKKMDLRKQRR	360						
Db	250	DEBIELEKLRISIVSGDPKKKYTFEKGASGVTYAMDVATGOEVAIKOMNLQQQPPK	309						

Qy	361	ELLFNEVVIMRDYOHENVENVMVNSVLVGDELVVVMEFLGGALTDIVTHTRMNEBQIAAV	4200
Db	310	ELIINEILVMRENKPNINVLNDSVLVGDELVVVVMYLAGSLTDVVTETCMDEGQIAAV	3699
Qy	421	CLAVLQALSVLHAQGVTHRDIKSDSIILTHDGRVKLSDFGCAOVSKVPPREKSLVGTPY	4800
Db	370	CRECLQALAEFLHSHQNVTHRDIKSDNIIILGMDGSKVLDTGFCQAQITPQSKRSTVMWGTPY	4299
Qy	481	WMAPELISRLPYGPEVDIWSIGIMVIEVMDGDEPPYFNFPPKAMKMRIDNLPRLKNLHK	540
Db	430	WMAPEVTVRKAYGPKVDIWSIGIMAIEMIEGEPYVLNENPLREALYLIATNGTPELQNPEK	4899
Qy	541	VSPSLKGFRLKLLVRDPAQRATAAEELKHPFLAKAGGPASIVPLM	585
Db	490	LSAIFRDFLNRLDMVDVEKRGSAKELLQHQLKIAKPLSLSTPLI	534

RESULT 7

S40482
serine/threonine-specific protein kinase (EC 2.7.1.1) - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C/Accession: S40482
R/Manser, E.; Leung, T.; Salihuddin, H.; Zhao, Z.; Lim, L.
Nature 367, 40-46, 1994
A/Title: A brain serine/threonine protein kinase activated by Cdc42 and Rac1.
A/Reference number: S40482; PMID:94150588; PMID:8107774

RESULT 7
S40482

serine/threonine-specific protein kinase (EC 2.7.1.1.) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S40482
R;Manser, E.; Leung, T.; Saliuddin, H.; Zhao, Z.; Lim, L.
Nature 367, 40-46, 1994
A;Title: A brain serine/threonine protein kinase activated by Cdc42 and Rac1.
A;Reference number: S40482; MUID:94150588; PMID:8107774
A;Accession: S40482
A;Molecule type: mRNA
A;Residues: 1-544 <MAN>
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;267-520/Domain: protein kinase homology <KIN>
F;275-283/Region: protein kinase ATP-binding motif

Query Match	28.9%;	Score 892;	DB 2;	Length 544;
Best Local Similarity	36.9%;	Pred. No. 1.5e-24;		
Matches 216;	Conservative	82;	Mismatches 165;	Indels 122;
				Gaps 11

QY	4	KRKRVEISAPSNFHRVHTGFDQHOEQKTGLPRQWOSLIEESARRPKPLVDPACITSIQ	63
Db	68	KEKERHIEISLPSDFEHTIHVGFDACTEFTCMPEQWALLQTSN	111
QY	64	PGAPKTIVRGSKGAKOGCALTLLLDEPENMSTVRSNLSLRDROSPPPPARAQENGMPBPAT	123
Db	112	-----ITKSEOKKNPQAVLDVLEFVNSKKT-SNSQKYS-----	144
QY	124	TARGPGPKAGSRGRFAGHSAGGSGDRRRAGPEKRPKSGREGGPOESSRDKRPLSGP	183
Db	145	-----FTDKSAEDYNSNTLNV-----KTVSETPAVPVSEDE-----	180
QY	184	DVCTPQAGLASAKLAAAGPFTN-----YPRADTDPHSGAOGEBHDVAPNGFSAGGLAIP	240
Db	181	DDATPPP-----VIAPRPHTKSYVTRSVI-----EPLVTPT-----	213
QY	241	QSSSSSRPPTRARGAPSPGVLPHASEPQLAPACTPAAPVPGPGPSRSPQRPQVS	300
Db	214	RDVATSPISPTENNTTP-----PDALTRNT-----EKQKKPKMS	248
QY	301	HEOFRAALQVDPDGPSPRSLDNFIKIGEGSTGIVCIATVRSGLKVAVKKMDLKRQORR	360
Db	249	DEILEKLRNIVSGDPKKYTRFEKIGQCSAGTVYVAMDVATGOEVAIKOMNLQOQPKK	308
QY	361	ELLFNEWIMRDYCHENVVMYNSYLVDGLVWVMEFLEGALTDIVTHTRMNEEQIAAV	420
Db	309	ELIINEILVMRENKNPNINYLDYSYLVDGLVWVMEYLAGSLTDVVTETCMDESGQIAAV	368
QY	421	CLAVLQALSVLHAQGYIHRDIKSDSILLTHDGRVKLSDFGFCQVSKSEVPRKXSLVGTFY	480
Db	369	CRECQALEFLHSNQVIMHRDIKSDNILLGMDGSKVLTDFGCAQITPEQKSRSTWVGTFY	428
QY	481	WMAPELISRLPYGPEVDIVSLGIMVJEMVDGPEPPFYNEPPLKAMKMTIRDNLPPRLKDLHK	540

Db 205 -----PQP 207
QY 173 SRRDKEPLSPDVGTPQAGLASGAKLAAGRPNTPYPRADTDHPSRGAQGEPHDVA PNGP 232
Db 208 YTSLSLPYHGNKIQDPRKNMPTTSTSSAG--YNS -----KQGV-----P 246
QY 233 SAGGLAIPSSSSSSRPPTTRARGAPSPGVGLPHASEP-OLAPPACTPAAPA-----282
Db 247 TTFVS-----NENRSSMPPSY---APP-----VPHGETPADIVPPA-IPDRPARTLSIYTKP 295
QY 283 -----VP-----GPPGPRS-PORPORVSHQEPRAALQIVVDGPRSYLDNFIKIGEGS 331
Db 296 KEEEEKIPLSKQGFQVARGQAKKMTDAEVLTKLRTIVSIGNDRKYRKVDKIGSGA 355
QY 332 TGIVCIATVSSSKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMYSYLVDGL 391
Db 356 SGSVYTAISISTAEVAIKQMLKQDPKKELLINEILVWRENKHANIVNLSYLVCDL 415
QY 392 WVMEFLEGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAGQVHHRDIKSDSILLTHD 451
Db 416 WVMEYLAGSLTDVVTEQMEDGIIAAVCREVLQALEFLHSRHHVHRDIKSDNILLGMD 475
QY 452 GRVKLSDFGFCQVSKVEVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLIGIMVMDVG 511
Db 476 GSVKLTDFGFCQVSKVEVPRKSLVGTPTWMAPEVTVTRKYQYGPKVDVWSLIGIMVMDVG 535
QY 512 EPPYNEPPLKAMKMRDNLPRLLKHLKVPSPSLKGLFDRLLVDRDPAQATAEILLKHPF 571
Db 536 EPPYNEPPLKAMKMRDNLPRLLKHLKVPSPSLKGLFDRLLVDRDPAQATAEILLKHPF 595
QY 572 LAKAGPPASIVPLM 585
Db 596 LRCAPLASLYYLI 609
RESULT 14
S60402
protein kinase CLA4 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein N0450; protein YNL0450; protein YNL298W
C:Species: Saccharomyces cerevisiae
C>Date: 27-Apr-1996 #sequence revision 17-May-1996 #text_change 24-Sep-1999
C:Accession: S60402; S63274; S53103
R:Maurer, K.C.T.; Urbanus, J.H.M.; Planta, R.J.
Yeast 11, 1303-1310, 1995
A:Title: Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV carrying a
C, and a novel putative serine/threonine protein kinase gene.
A:Reference number: S60394; MUID:96132033; PMID:8553702
A:Accession: S60402
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-842 <MAU>
A:Cross-references: EMBL:U23084; NID:g1050853; PIDN:AAC49100.1; PID:g1050862
R:Maurer, C.T.C.; Urbanus, J.H.M.; Planta, R.J.
Submitted to the Protein Sequence Database, April 1996
A:Reference number: S63266
A:Accession: S63274
A:Molecule type: DNA
A:Residues: 1-842 <MAU>
A:Cross-references: EMBL:Z71574; NID:g1302389; PIDN:CAA96216.1; PID:e239731; PID:g130239
A:Experimental source: strain S288C
R:Chvrkova, F.; Naemlyth, K.
Submitted to the EMBL Data Library, November 1994
A:Description: STE20-like protein kinases are required for cytokinesis.
A:Reference number: S53103
A:Accession: S53103
A:Molecule type: DNA
A:Residues: 1-389, 1', 391-842 <CVR>
A:Cross-references: EMBL:X82499; NID:g732943; PIDN:CAA57879.1; PID:g732944
A:Experimental source: strain K1107
C:Genetics:
A:Gene: SGD: CLA4; ERC10
A:Cross-references: SGD:S0005242; MIPS:YNL298W

A:Map position: 14L
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; pleckstrin repeat hom
C:Keywords: ATP; phosphotransferase
F:544-825/Domain: protein kinase homology <KIN>
Query Match 24.6%; Score 760; DB 2; Length 842;
Best Local Similarity 31.2%; Pred. No. 7.6e-20;
Matches 212; Conservative 99; Mismatches 239; Indels 130; Gaps 23;
QY 11 ISAPSNFHRVHTGDDHQEQKFTGLPRQWSLIESARRPKPLVD--PACISIQ-----63
Db 184 VSSPTNFTKHVGDPEPTGSEFVGMPTNWEKLLKHSRITCEDWNNSAAVIOVLQFYQBY 243
QY 64 --PGAPKTVIRGSKGAKGKALILLDEPENMVSVTRNSL-----RDSPP 106
Db 244 NGAGNPTNTLDQSGETSSSKSLPNSYNDKLNNSVNSKSSGVSVMVSQRTKSIP 303
QY 107 PPARARQENG-----MPEEPATTAR---GGPGKAGSRGRFAGHSEAGGSGDRRR 153
Db 304 PNTKGFVSLGSLPPIINTKLPTSQSNIPRLQNVNPNQYPKMR-NGHSPFNG---QFP 358
QY 154 AGPEKPKSSRSGSGGPGQESSRDKP-----LSGPDVGTTPQAGLAGAKLAAGRPN 206
Db 359 RGMHPNNSQRSLOQQQQQQQQKQHQYYPYHQQP---SPSPSPSPS-----PLN 407
QY 207 TYPRADTDHPSRGAQGEPHDVA PNGP---SAGGLAIPSSSSSSSRPPTRA-----RGAP 257
Db 408 PY-----RPHN-MINPYSKOPQPLSSQSTQNOAIPRYAQNSS--PTAAHFPOORTAP 458
QY 258 SPGVGLPHASEPQ-----LAP-----PACTPAAPAVP---GPGGPRSPQRE 295
Db 459 KPPIISAPRAPYPSNQNSATSNTHVQVPAPKNDQSTPTQMRQAPKRPDADVAQGGVAKPKK 518
QY 296 POR--VSHEQFRAALQIVVDGPRSYLDNFIKIGEGSTGIVCIA-----TVRSS-----343
Db 519 PARPTMSTAETMSKLVKVTYNADPSQCFKVIKAGQAGSGSYLAERTHIPTESNMIELI 578
QY 344 -----GKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMYSYL-VGDELWV 393
Db 579 NNDIDEPHVGDVKVAKQVLSKQPKELIVNELLWKSRRHKNIVNFEAYLRTDLDLWV 638
QY 394 VMFEGGALTDIV-----THTRMNEEQIAAACLAVLQALSVLHAGQVHHRDIKSDS 445
Db 639 VMFMEGGSLTDIIENSPTNDNSHPLTEPQIAYIVRETQGLKFLHDKHIIHRDIKSDN 698
QY 446 ILLTHDGVKLSDFGFCQVSKVEVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLIGIMV 505
Db 699 VLLDTRARVKITDFGFCARLTDKRSKRATMVGTPYWMAPEVVKQREYDEKIDVWSLIGIMT 758
QY 506 IMVDGEPYPYFNEPPLKAMKMRDNLPRLLKHLKVPSPSLKGLFDRLLVDRDPAQATAAE 565
Db 759 IEMLEGEPPYLNEDPLKALYLIATNGTFLKHKHPESLSLEIKRFLSVCLVDVRYRASTEE 818
QY 566 LKHPFLAKAGPPASIVPLM 585
Db 819 LLHHGFFNMACDPKDLTSLI 838
RESULT 15
T26684
hypothetical protein Y38F1A.10 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T26684
R:Wallis, J.
Submitted to the EMBL Data Library, October 1998
A:Reference number: Z20253
A:Accession: T26684
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-378 <WIL>
A:Cross-references: EMBL:AL032639; PIDN:CAA21637.1; GSPDB:GN000020; CESP:Y38F1A.10
A:Experimental source: clone Y38F1A

C:Genetics:
A:Gene: CESP:X38F1A.10
A:Map position: 2
A:Introns: 43/3; 221/2; 259/2; 309/3; 347/2
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 23.4%; Score 722; DB 2; Length 378;
Best Local Similarity 45.3%; Pred. No. 8.2e-19;
Matches 143; Conservative 61; Mismatches 110; Indels 2; Gaps 2;

QY	277	TPAAPVPGPPGPGSPQREPKRVSHQFRAALQLVVDPDPRSILDNFIKIGEGSTGIVC	336
DB	64	TTVEPPPEEPVVRASHREKLSDEVLNQLREIVNPSNPLGKYEKKQIGVGASGTVF	123
QY	337	IATVRSSGKLNAVKKMDLRKQRRRELLFNEVVIMRDYQHENVVEMNSYLV-GDELWVVM	395
DB	124	VANVAGSTDVVAVKRMFAKTPQKEMLLTEIKVMKQYRHPNLVNYIESYLVADADDLWVVM	183
QY	396	EFLEGGALTDIVHTRMNEEQIAAVCLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVK	455
DB	184	DYLEGGNLTDDVVVKTELDGQIAAVLQECALKALHFLHRHSIVHRDIKSDNVLGMNGEVK	243
QY	456	LSDFGFCQVSKVPRRKSLVGTPTVWMAPELISRLPYGPEVDIWSLGINVIMVNDGEPPY	515
DB	244	LTDMGFCAQI-QPGSKRDIVVGTPTVWMSPEILNKQYNYKVDIWSLGINALEMIDGEPY	302
QY	516	FNEPPLKAMKMTIRDNLPRLKNLHKVSPSLKGLDRLVDPQARATAAEILKHPFLAKA	575
DB	303	LRETPLKATYLIAQNGKPEIKQDRLSSEFNFLDKLVDPDQADTTTELLAHPFLKKA	362
QY	576	GPPASIVPLMRQNTR	591
DB	363	KPLSSLIPYIRAVREK	378

Search completed: September 29, 2004, 18:05:37
Job time : 47.4559 secs

Blank

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 17:41:57 ; Search time 133.844 Seconds
(without alignments)
1393.197 Million cell updates/sec

Title: US-10-693-367-2

Perfect score: 3090

Sequence: 1 MFGKKRKRVEISAFNSFEHR.....LAKAGPPASIVPLMRQNRTR 591

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2860	92.6	593	11 Q8BTW9	Q8btw9 mus musculus
2	2853	92.3	593	11 Q80Z97	Q80z97 mus musculus
3	2558	82.8	501	4 Q8N4E1	Q8n4e1 homo sapien
4	2202.5	71.3	467	4 Q9ULS8	Q9uls8 homo sapien
5	2202.5	71.3	483	4 Q8NDE3	Q8nde3 homo sapien
6	2124.5	68.8	650	13 Q90W62	Q90w62 xenopus lae
7	1967	63.7	407	11 Q8K0U2	Q8k0u2 mus musculus
8	1748	56.6	719	11 Q8C015	Q8c015 mus musculus
9	1740	56.3	719	11 Q8BVB0	Q8bvb0 mus musculus
10	1731	56.0	719	4 Q8TB93	Q8tb93 homo sapien
11	1501.5	48.6	639	5 Q9VXE5	Q9vxe5 drosophila
12	1497.5	48.5	639	5 Q960J8	Q960j8 drosophila
13	1497.5	48.5	639	5 Q96372	Q96372 drosophila
14	1241	40.2	240	4 Q8NCH5	Q8nch5 homo sapien
15	1160	37.5	229	11 Q9CS71	Q9cs71 mus musculus
16	1096.5	35.5	540	5 Q9U3M1	Q9u3m1 caenorhabdi

ALIGNMENTS

RESULT 1

ID	Q8BTW9	PRELIMINARY;	PRT;	593 AA.
AC	Q8BTW9;			
DT	01-MAR-2003 (Tremblrel. 23, Created)			
DT	01-MAR-2003 (Tremblrel. 23, Last sequence update)			
DE	01-OCT-2003 (Tremblrel. 25, Last annotation update)			
DE	Serine/threonine-protein kinase PAK 4 (Similar to			
DE	p21(CDKN1A)-activated kinase 4).			
GN	PAK4 OR 5730488L07RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NOD; TISSUE=Thymus;			
RX	MEDLINE=22354683; PubMed=12466851;			
RA	The FANTOM Consortium,			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs."			
RL	Nature 420:563-573(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FVB/N; TISSUE=Colon;			
RA	Strausberg R.;			
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK088512; BAC40396.1; -			
DR	EMBL; BC048238; AHA48238.1; -			
DR	MGD; MGI:1917834; Pak4.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.			
DR	GO; GO:0004674; F:protein-tyrosine kinase activity; IEA.			
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	InterPro; IPR000035; PAKbox/Rho-binding.			
DR	InterPro; IPR000719; Prot_kinase.			
DR	InterPro; IPR002290; Ser_thr_kinase.			
DR	InterPro; IPR001245; Tyr_kinase.			

Q18637 caenorhabdi
Q9vi13 drosophila
Q24190 drosophila
Q24213 drosophila
Q8kl16 mus musculu
Q80320 brachydanio
Q8kl15 mus musculu
Q8axb4 xenopus lae
Q8cin4 mus musculu
Q72328 homo sapien
Q7yql4 pan troglod
Q7yql3 pongo pygma
Q8aw67 brachydanio
Q9p0j8 homo sapien
Q9gyu0 rattus norv
Q8l9c2 xenopus lae
Q728e9 magnaporthe
Q9yeb5 homo sapien
Q96uh9 magnaporthe
Q75561 homo sapien
Q9pw62 xenopus lae
Q13431 candida alb
Q9hew4 cryptococcu
Q57318 xenopus lae
Q8nk62 ustilago ma
Q8xlf0 cryptococcu
Q9p496 yarrowia li
Q9hew5 cryptococcu
Q9uv59 cryptococcu

DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S.TKG; 1.
 DR SMART; SM00219; TyrKG; 1.
 DR PROSITE; PS0108; CRIB; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 KW Kinase.
 SQ SEQUENCE 593 AA; 64622 MW; 4AFA91DD73D4C6D5 CRC64;
 Query Match 92.6%; Score 2860; DB 11; Length 593;
 Best Local Similarity 92.6%; Pred. No. 4.6e-191;
 Matches 550; Conservative 10; Mismatches 30; Indels 4; Gaps 2;
 QY 1 MFGKKKEVEISAPSNFHRVHTGPDQHEQKFTGLPRQWSLIESARRPKPLVDPAICIT 60
 Db 1 MFGKKKEVEISAPSNFHRVHTGPDQHEQKFTGLPRQWSLIESARRPKPLVDPAICIT 60
 QY 61 SIQGPAPKTIVRGSKGAKDGLTLLDDEFNMSVTRSNLSRRDPPPPARARQENMPPEE 120
 Db 61 SIQGPAPKTIVRGSKGAKDGLTLLDDEFNMSVTRSNLSRRDPPPPARARQENMPPEE 120
 QY 121 PATTARGGPGKAGSRGPFAGHSEAGGSGDRRRRAGPEKPKSSREGSGGPOESSDKRPL 180
 Db 121 RAAPARMADPKAGSRARATGHSEAGSGGDRRRRVGPEKPKSSRDGPGQEQASRDKRPL 180
 QY 181 SGPDVGTTPQAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEPHDVA PNGSAGGLAIP 240
 Db 181 SGPDVSTTPQGSLSGTGLAAGRPNTPYPRADTDHPPRGAQGEPTMAPNGPSATGLAIP 240
 QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPQLAPPA---CTPAAPAVPGPPGPRSPQRPQ 297
 Db 241 Q---SSSSSRPPTRARGAPSPGVLGPHASEPQLAPPA---CTPAAPAVPGPPGPRSPQRPQ 299
 QY 298 RVSHQFRAALQLVVDGDPKSYLDNFKIKGEGSTGIVCIATVRSSGKLVAVKMDLRKQ 357
 Db 300 RVSHQFRAALQLVVDGDPKSYLDNFKIKGEGSTGIVCIATVRSSGKLVAVKMDLRKQ 359
 QY 358 QRRELLFNEVIMRDYQHENVNMYNSYLVDGLVWVMEFLEGGALTDIVTHTRNNEQI 417
 Db 360 QRRELLFNEVIMRDYQHENVNMYNSYLVDGLVWVMEFLEGGALTDIVTHTRNNEQI 419
 QY 418 AAVCLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGFCQAQVSKVEPRKSLVG 477
 Db 420 AAVCLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGFCQAQVSKVEPRKSLVG 479
 QY 478 TPYWMAPELISRLPYGPEVDIWSLIGIMVEMVDGEPYFNEPPLKAMQWIRDNLPRLKN 537
 Db 480 TPYWMAPELISRLPYGPEVDIWSLIGIMVEMVDGEPYFNEPPLKAMQWIRDNLPRLKN 539
 QY 538 LHKVSPSLKGLDRLLRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
 Db 540 LHKASPSLKGFLDRLLRDPAQRATAAELLKHPFLTKAGPPASIVPLMRQNRTR 593

RESULT 2

Q80297 ID Q80297 PRELIMINARY; PRT; 593 AA.
 AC Q80297;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAIB/C;
 FX MEDLINE=22526742; PubMed=12529371;

RESULT 3
 Q8N4E1

RA Lu Y., Pan Z.Z., Devaux Y., Ray P.;
 RT "p21-activated Protein Kinase 4 (PAK4) Interacts with the Keratinocyte
 RT Growth Factor Receptor and Participates in Keratinocyte Growth Factor-
 RT mediated Inhibition of Oxidant-induced Cell Death.";
 RL J. Biol. Chem. 278:10374-10380 (2003).
 DR EMBL; AY217016; AAC61496.1; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000095; PAKbox/RhoBndng.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S.TKG; 1.
 DR SMART; SM00219; TyrKG; 1.
 DR PROSITE; PS0108; CRIB; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 KW Kinase.
 SQ SEQUENCE 593 AA; 64666 MW; D7B3BD36706BAF4 CRC64;
 Query Match 92.3%; Score 2853; DB 11; Length 593;
 Best Local Similarity 92.6%; Pred. No. 1.4e-190;
 Matches 550; Conservative 9; Mismatches 31; Indels 4; Gaps 2;
 QY 1 MFGKKKEVEISAPSNFHRVHTGPDQHEQKFTGLPRQWSLIESARRPKPLVDPAICIT 60
 Db 1 MFGKKKEVEISAPSNFHRVHTGPDQHEQKFTGLPRQWSLIESARRPKPLVDPAICIT 60
 QY 61 SIQGPAPKTIVRGSKGAKDGLTLLDDEFNMSVTRSNLSRRDPPPPARARQENMPPEE 120
 Db 61 SIQGPAPKTIVRGSKGAKDGLTLLDDEFNMSVTRSNLSRRDPPPPARARQENMPPEE 120
 QY 121 PATTARGGPGKAGSRGPFAGHSEAGGSGDRRRRAGPEKPKSSREGSGGPOESSDKRPL 180
 Db 121 RAAPARMADPKAGSRARATGHSEAGSGGDRRRRVGPEKPKSSRDGPGQEQASRDKRPL 180
 QY 181 SGPDVGTTPQAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEPHDVA PNGSAGGLAIP 240
 Db 181 SGPDVSTTPQGSLSGTGLAAGRPNTPYPRADTDHPPRGAQGEPTMAPNGPSATGLAIP 240
 QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPQLAPPA---CTPAAPAVPGPPGPRSPQRPQ 297
 Db 241 Q---SSSSSRPPTRARGAPSPGVLGPHASEPQLAPPA---CTPAAPAVPGPPGPRSPQRPQ 299
 QY 298 RVSHQFRAALQLVVDGDPKSYLDNFKIKGEGSTGIVCIATVRSSGKLVAVKMDLRKQ 357
 Db 300 RVSHQFRAALQLVVDGDPKSYLDNFKIKGEGSTGIVCIATVRSSGKLVAVKMDLRKQ 359
 QY 358 QRRELLFNEVIMRDYQHENVNMYNSYLVDGLVWVMEFLEGGALTDIVTHTRNNEQI 417
 Db 360 QRRELLFNEVIMRDYQHENVNMYNSYLVDGLVWVMEFLEGGALTDIVTHTRNNEQI 419
 QY 418 AAVCLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGFCQAQVSKVEPRKSLVG 477
 Db 420 AAVCLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGFCQAQVSKVEPRKSLVG 479
 QY 478 TPYWMAPELISRLPYGPEVDIWSLIGIMVEMVDGEPYFNEPPLKAMQWIRDNLPRLKN 537
 Db 480 TPYWMAPELISRLPYGPEVDIWSLIGIMVEMVDGEPYFNEPPLKAMQWIRDNLPRLKN 539
 QY 538 LHKVSPSLKGLDRLLRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
 Db 540 LHKASPSLKGFLDRLLRDPAQRATAAELLKHPFLTKAGPPASIVPLMRQNRTR 593

ID Q8N4E1 PRELIMINARY; PRT; 501 AA.
 AC Q8N4E1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to RIKEN cDNA 5730488L07 gene.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RC Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC034511; AAH34511.1; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferrase activity; IEA.
 DR GO; GO:0008468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000095; PAKBox/RhoBndng.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00219; TyTKC; 1.
 DR PROSITE; PS50108; CRIB; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Transferase.
 SQ SEQUENCE 501 AA; 54940 MW; 6EE6240ECB65E79D CRC64;

Query Match 82.8%; Score 2558; DB 4; Length 501;
 Best Local Similarity 84.8%; Pred. No. 4.2e-170;
 Matches 501; Conservative 0; Mismatches 0; Indels 90; Gaps 1;
 QY 1 MFGKRRKRVIEISAPSNFHRVHTGFQHEQKFTGLPRQMSLIEESARRPKPLVDPAKIT 60
 DB 1 MFGKRRKRVIEISAPSNFHRVHTGFQHEQKFTGLPRQMSLIEESARRPKPLVDPAKIT 60
 QY 61 SIQPGAPKTIIVRGSKGAKGKALTLTLLDEFNMSVTRSNLSLRDSDPPPPARARQENGMP 120
 DB 61 SIQPGAPKTIIVRGSKGAKGKALTLTLLDEFNMSVTRSNLSLRDSDPPPPARARQENGMP 120
 QY 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRAGPEKPKSRREGSGGPGQESSRDKRPL 180
 DB 121 PATTARGGPGK----- 131
 QY 181 SGPDVGTPOAGLAKGAKLAAGRPNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
 DB 132 -----GEPHDVAPNGPSAGGLAIP 150
 QY 241 QSSSSSRPPTARGAPSPGVLGPHASEPOLAPACTPAAPAVGPGPPSPQREPORVS 300
 DB 151 QSSSSSRPPTARGAPSPGVLGPHASEPOLAPACTPAAPAVGPGPPSPQREPORVS 210
 QY 301 HEQFRAALQVLVDGPRSLVDNFIKIGEGSTGIVCIATVRSKGLVAVKMDLRKQORR 360
 DB 211 HEQFRAALQVLVDGPRSLVDNFIKIGEGSTGIVCIATVRSKGLVAVKMDLRKQORR 270
 QY 361 ELLFNEVIMRDYQHENVNMYNSYLVGDELVWVMEFLEGALTDIVTHTRMNEEQIAAV 420
 DB 271 ELLFNEVIMRDYQHENVNMYNSYLVGDELVWVMEFLEGALTDIVTHTRMNEEQIAAV 330
 QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGFCQVSKVEVPRKSLVGTPT 480
 DB 331 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGFCQVSKVEVPRKSLVGTPT 390

QY 481 WWAPELISRLPYGPEVDIWSLGIWVIEVMDGEPYPFNEPPLKAMKQVIRDNLPPRLKNLHK 540
 DB 391 WWAPELISRLPYGPEVDIWSLGIWVIEVMDGEPYPFNEPPLKAMKQVIRDNLPPRLKNLHK 450
 QY 541 VSPSLKGLFDRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
 DB 451 VSPSLKGLFDRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 501
 RESULT 4
 Q9ULS8
 ID Q9ULS8 PRELIMINARY; PRT; 467 AA.
 AC Q9ULS8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein KIAA1142 (Fragment).
 GN KIAA1142.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RC MEDLINE=20039618; PubMed=10574461;
 RA Hiroseawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
 RT "Characterization of cDNA clones selected by the Genemark analysis
 from size-fractionated cDNA libraries from human brain.";
 RL DNA Res. 6:329-336(1999).
 DR EMBL; AB032968; BAA86456.1; -.
 DR HSP; Q63450; 1A06.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferrase activity; IEA.
 DR GO; GO:000468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000095; PAKBox/RhoBndng.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS50108; CRIB; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Hypothetical protein; ATP-binding; Transferase.
 FT NON TER 1
 SQ SEQUENCE 467 AA; 51464 MW; EC342B8F5C5E3940 CRC64;
 Query Match 71.3%; Score 2202.5; DB 4; Length 467;
 Best Local Similarity 74.1%; Pred. No. 2.3e-145;
 Matches 438; Conservative 0; Mismatches 0; Indels 153; Gaps 1;
 QY 1 MFGKRRKRVIEISAPSNFHRVHTGFQHEQKFTGLPRQMSLIEESARRPKPLVDPAKIT 60
 DB 30 MFGKRRKRVIEISAPSNFHRVHTGFQHEQKFTGLPRQMSLIEESARRPKPLVDPAKIT 89
 QY 61 SIQPGAPKTIIVRGSKGAKGKALTLTLLDEFNMSVTRSNLSLRDSDPPPPARARQENGMP 120
 DB 90 SIQPGAPK----- 97
 QY 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRAGPEKPKSRREGSGGPGQESSRDKRPL 180
 DB 98 ----- 97
 QY 181 SGPDVGTPOAGLAKGAKLAAGRPNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
 DB 98 -----GEPHDVAPNGPSAGGLAIP 116
 QY 241 QSSSSSRPPTARGAPSPGVLGPHASEPOLAPACTPAAPAVGPGPPSPQREPORVS 300

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Db 117 QSSSSSRPPTTRARGAPSGVLGPHASEPQLAPPACTPAAPVAVPGPPGPRSPQRPQVRS 176
QY 301 HEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQRR 360
Db 177 HEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQRR 236
QY 361 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 420
Db 237 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 296
QY 421 CLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRPKSLVGTTPY 480
Db 297 CLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRPKSLVGTTPY 356
QY 481 WNAPELISRLPYGPEVDIWSLGIWVEMVDGPPYFNEPPLKAMKMWIRNLPRLKNLHK 540
Db 357 WNAPELISRLPYGPEVDIWSLGIWVEMVDGPPYFNEPPLKAMKMWIRNLPRLKNLHK 416
QY 541 VSPSLKGFLLRLLVRDPAQRTAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
Db 417 VSPSLKGFLLRLLVRDPAQRTAAELLKHPFLAKAGPPASIVPLMRQNRTR 467

RESULT 5
QND33
ID Q8NDE3 PRELIMINARY; PRT; 483 AA.
AC Q8NDE3;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFPZ547G182.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834236; CAD38914.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/RhoGing.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
KW Hypothetical protein, ATP-binding, Transferase.
FT NON_TER
SQ SEQUENCE 483 AA; 52787 MW; 8976E3BF0B8818B6 CRC64;

Query Match 71.3%; Score 2202.5; DB 4; Length 483;
Best Local Similarity 74.1%; Pred. No. 2.4e-145;
Matches 438; Conservative 0; Mismatches 0; Indels 153; Gaps 1;

QY 1 MFGKKRKEVEISAPSNFHRVHTGPDQHQKFTGLPQWQSLIESARRPKPLVDPACIT 60
Db 46 MFGKKRKEVEISAPSNFHRVHTGPDQHQKFTGLPQWQSLIESARRPKPLVDPACIT 105
QY 61 SIQPGAPKTIYVSGKAGDKGALTLLDEFENSVTRNSLRDSDPPPPARARQENGMPPEE 120

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Db 106 SIQPGAPK----- 113
QY 121 PATTARGGPGKAGSRGRTFAGHSEAGGGGDRRRAGPEKPKSRSGSGGPGQESSRDKRPL 180
Db 114 ----- 113
QY 181 SGPDVGTTPQAGLASGAKLAAGRPNFTYPRADTDHPSRGAQGEHPHDVAPNGPSAGGLATP 240
Db 114 -----CEPHDVAPNGPSAGGLATP 132
QY 241 QSSSSSRPPTTRARGAPSGVLGPHASBPQLAPPACTPAAPVAVPGPPGPRSPQRPQVRS 300
Db 133 QSSSSSRPPTTRARGAPSGVLGPHASBPQLAPPACTPAAPVAVPGPPGPRSPQRPQVRS 192
QY 301 HEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQRR 360
Db 193 HEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQRR 252
QY 361 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 420
Db 253 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 312
QY 421 CLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRPKSLVGTTPY 480
Db 313 CLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRPKSLVGTTPY 372
QY 481 WNAPELISRLPYGPEVDIWSLGIWVEMVDGPPYFNEPPLKAMKMWIRNLPRLKNLHK 540
Db 373 WNAPELISRLPYGPEVDIWSLGIWVEMVDGPPYFNEPPLKAMKMWIRNLPRLKNLHK 432
QY 541 VSPSLKGFLLRLLVRDPAQRTAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
Db 433 VSPSLKGFLLRLLVRDPAQRTAAELLKHPFLAKAGPPASIVPLMRQNRTR 483

RESULT 6
Q90W62
ID Q90W62 PRELIMINARY; PRT; 650 AA.
AC Q90W62;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE PAK5 protein.
GN PAK5.
OS Xenopus laevis (African clawed frog)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RA Cau J., Faure S., Delsert C., Morin N.;
RT "A novel xenopus p21 activated kinase expressed in brain.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277826; CAC40979.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/RhoGing.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
KW ATP-binding; Transferase.

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SQ SEQUENCE 650 AA; 73736 MW; 9274DC6CACD4A081 CRC64;
Query Match 68.8%; Score 2124.5; DB 13; Length 650;
Best Local Similarity 66.4%; Pred. No. 9.5e-140;
Matches 442; Conservative 43; Mismatches 90; Indels 91; Gaps 13;
QY 1 MFGKKKVEISAPNFEHVRHTGFDQEQKFTGLPQWQSLIESARRKPLVDPAIC 60
DB 1 MFAKKKVEISAPNFEHVRHTGFDQEQKFTGLPQWQSLIESARRKPLVDPSYIT 60
QY 61 STQGPAPKTIVRGSKGAKDGLTLLDEFENMSVTRSNLSRDSPP---PPPARAQENGM 117
DB 61 TIKHVPQKTIVRGNKSLDGLLDEFDDMSVCRSNLSRDSPPCPQREGRFHQENGM 120
QY 118 PE-----EPATTARGG----- 128
DB 121 SEVRVROQREDQGRSERNRSEHRRERQREHRAVPOQPGQEPSNKHRRPPPPYPKDI 180
QY 129 PGKAGSRGRFAGHSBAGG-----GSGD-----RRRAGPEKRPKSS-REGSGGPOE 172
DB 181 PEKRGPR---SHEKSDGRREYPCNDRGHSDPVERVVKDKGEEKRPSKAYSITSGESQP- 235
QY 173 SSRDKRPLSGDVGTPQAGLASGAK-LAAGRPFNTPYPRADTDHPSRGAQGEHVDVAPNG 231
DB 236 SPRDKRPLSGPNIRTPGSSSTDGVVVKQTETGRPFNTYPRAEVD-PNRGAHQVSDSRSTV 294
QY 232 P-----SAGGLAIQSSSSSRPPTTRARGAPSPGVLGPHASEPOLAPACTPAAPAVPG 285
DB 295 PLDSKSSVSKGSSRPQGGQVKKPPEK-----PHPTQLAPHSSDPQLSRPVQT-----QH 344
QY 286 PPGPSPQEPQVSHQEPRAALQLVDPGDRPSYLDNFIKIGEGSTGIVCIATVRSSGK 345
DB 345 PAQPSQEPQVSHQEPRAALQVDPGDRPTVLDNFIKIGEGSTGIVCIATIKSSGK 404
QY 346 LVAVKMDLRKQORRELLFNVEVVRDYQHENVVEMVNSYLVGDELWVMEFLEGGALTD 405
DB 405 LVAVKMDLRKQORRELLFNVEVVRDYQHENVVEMVNSYLVGDELWVMEFLEGGALTD 464
QY 406 IVTHTRMNEEQIAANCLAVLQALSVLHAQGVHTRDKSDSILLTHDGRVKLSDFGFCACV 465
DB 465 IVTHTRMNEEQIATCVSVLKAQGVHTRDKSDSILLTHDGRVKLSDFGFCACV 524
QY 466 SKVPRKSLVGTTPYMAPELISRLPYGPEVDIWSLGIWVEMVDEGEPYFNEPPLKAMK 525
DB 525 NKEVPARKSLVGTTPYMAPELISRLPYGPEVDVWSLGIWVEMVDEGEPYFNEPPLKAMK 584
QY 526 MIRDNLPPRLKXNKHVSPSLKGFDRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLM 585
DB 585 MIRDNLPPKNAQKVSPLKGFDRLLVRDPSQASANELLKHPFLKAGPPSCIVPLM 644
QY 586 QONRTR 591
DB 645 QONRMR 650

RESULT 7
Q8K0U2 PRELIMINARY; PRT; 407 AA.
ID Q8K0U2
AC Q8K0U2
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN PAK4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX The FANTOM Consortium;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC030389; AAH30389.1; -.
DR MGI; 1917834; Pak4.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; ATP-binding; Transferase.
FT NON_TER 1
SQ SEQUENCE 407 AA; 44339 MW; 921689734DF9D710 CRC64;
Query Match 63.7%; Score 1967; DB 11; Length 407;
Best Local Similarity 94.5%; Pred. No. 5e-129;
Matches 380; Conservative 5; Mismatches 13; Indels 4; Gaps 2;
QY 193 LASGAKLAAGRPFNTPYPRADTDHPSRGAQGEHVDVAPNGPSAGGLAIQSSSSSRPPTTR 252
DB 7 LTSGTKLAAGRPFNTPYPRADTDHPSRGAQGEHVDVAPNGPSATGLAAPQ-SSSSSRPPTTR 65
QY 253 ARGAPSPGVLGPHASEPOLAPPA---CTPAAPAVPGPGRSPQEPQVSHQEPRAALQ 309
DB 66 ARGAPSPGVLGPHASEPOLAPPAALAAAPAVPAPFPGPGRSPQEPQVSHQEPRAALQ 125
QY 310 LVVDPGDRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNVEVI 369
DB 126 LVVDPGDRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNVEVI 185
QY 370 MRDYQHENVVEMVNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAANCLAVLQAL 429
DB 186 MRDYQHENVVEMVNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAANCLAVLQAL 245
QY 430 VLHAQGVHTRDKSDSILLTHDGRVKLSDFGFCACVSKVEPVRKSLVGTTPYMAPELISR 489
DB 246 VLHAQGVHTRDKSDSILLTHDGRVKLSDFGFCACVSKVEPVRKSLVGTTPYMAPELISR 305
QY 490 LPYGPEVDIWSLGIWVEMVDEGEPYFNEPPLKAMKMDNLPRLKXNKHVSPSLKGF 549
DB 306 LPYGPEVDIWSLGIWVEMVDEGEPYFNEPPLKAMKMDNLPRLKXNKHVSPSLKGF 365
QY 550 DRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
DB 366 DRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 407

RESULT 8
Q8C015 PRELIMINARY; PRT; 719 AA.
ID Q8C015
AC Q8C015
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Serine/threonine-protein kinase PAK 5.
GN 2900083L08RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of

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RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK032593; BAC27939.1; -.
DR MGD; MGI:1920334; 2900083L08Rik.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/RhoGndg.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
SQ SEQUENCE 719 AA; 80948 MW; 5E16D2318C238C8D CRC64;

Query Match 56.6%; Score 1748; DB 11; Length 719;
Best Local Similarity 52.9%; Pred. No. 1.9e-113;
Matches 385; Conservative 65; Mismatches 128; Indels 150; Gaps 16;

QY 1 MFGKKKRVETISAPNFHRVHTGFDQHEQKFTGLPRWQSLIESARRPKPLVDPACIT 60
Db 1 MFGKKKKIELSISPENFHRVHTGFDQEQKFTGLPQOWHSLADTANRPKPMVDPSCIT 60

QY 61 SIQGPACTIVRGSKGAKDGLTLLDEFENMVSRTNSLRDSDPPP-ARAR-112
Db 61 PIQLAPMKTIVRGNSCKETSINGLEDNFNISVTRNSLRKESPTPDQGAASRIQHS 120

QY 113 QENGM-----PEPATATARGGPKAGSRGFA-----GH-----141
Db 121 EENGFIITFSQYSSESDDTADYTTTEKYRDRSLYGGDLDLYKSSHAAKQNGHAMKMGHGA 180

QY 142 -----SEAGGSGDRRA-----154
Db 181 YYPEMKSILKTDLAGFPVVDYHDLTLDRKESYEGLRWYDQFASSSPLDYSPQLTPSRTA 240

QY 155 -----EKRPKSREGSGGFGQESSRDRKRLPLSGDVGTP-QPA 191
Db 155 -----EKRPKSREGSGGFGQESSRDRKRLPLSGDVGTP-QPA 191

60 650 QAMRRIRDSLPVRKDLHKVSMLRGFLDMLVREPSQRATAQELLGHFPLKLAGPPSCI 709
QY 582 VPLMRQNR 589
Db 710 VPLMRQYR 717

RESULT 9
QY Q8BVBO PRELIMINARY; PRT; 719 AA.
ID Q8BVBO;
AC Q8BVBO;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Serine/threonine-protein kinase PAK 5.
GN 2900083L08Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002).
DR EMBL; AK079080; BAC37528.1; -.
DR MGD; MGI:1920334; 2900083L08Rik.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/RhoGndg.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
SQ SEQUENCE 719 AA; 80967 MW; F1E33DCB8C39875B CRC64;

Query Match 56.3%; Score 1740; DB 11; Length 719;
Best Local Similarity 52.7%; Pred. No. 6.8e-113;
Matches 384; Conservative 65; Mismatches 129; Indels 150; Gaps 16;

QY 1 MFGKKKRVETISAPNFHRVHTGFDQHEQKFTGLPRWQSLIESARRPKPLVDPACIT 60
Db 1 MFGKKKKIELSISPENFHRVHTGFDQEQKFTGLPQOWHSLADTANRPKPMVDPSCIT 60

QY 61 SIQGPACTIVRGSKGAKDGLTLLDEFENMVSRTNSLRDSDPPP-ARAR-112
Db 61 PIQLAPMKTIVRGNSCKETSINGLEDNFNISVTRNSLRKESPTPDQGAASRIQHS 120

QY 113 QENGM-----PEPATATARGGPKAGSRGFA-----GH-----141
Db 121 EENGFIITFSQYSSESDDTADYTTTEKYRDRSLYGGDLDLYKSSHAAKQNGHAMKMGHGA 180

QY 142 -----SEAGGSGDRRA-----154
Db 181 YYPEMKSILKTDLAGFPVVDYHDLTLDRKESYEGLRWYDQFASSSPLDYSPQLTPSRTA 240

QY 155 -----EKRPKSREGSGGFGQESSRDRKRLPLSGDVGTP-QPA 191
Db 155 -----EKRPKSREGSGGFGQESSRDRKRLPLSGDVGTP-QPA 191

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Db      241 GTSRCKESLAYSESDWGPSLDDRRPKSYLHOTSQPMR-QRSKSGSLQEPMPMF 299
      192 GLSAGAKLAAGRPNTY-----PRADTDH-----PSRGAQGEHVDVAPNGP 232
      300 GASAFKTHPQGHSYNSYTPRLSEPTMCPKVVDYDRAQWVSPPLSGS-----DTYPRGP 354
      233 SAGGLAIPOS-----SSSSRPPTRARGA-----PSGVLGPHASEPQLAPPACTPAAP 281
      355 T-----KLPSQSKAGYSGSHQYPSGYHKASLYHHPSLQTSQYISTASYL-SSLSISS 409
      282 AVPGPGPRSPQREPORVSHEQFRAALQVLVDGDPGRSYLONFIKIGEGSTGIVCIATVR 341
      410 TYPSPSGSSSDQPSRVSHQFRAALQVLVSPGDPREYLNFIKIGEGSTGIVCIATEK 469
      342 SSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLGG 401
      470 HTGKQAVKMDLRKQORRELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLGG 529
      402 ALTDIVTHTRMNEEQIAAACLAVLOALSVLHQAQGVHHRDIKSDSILLTHDGRVKLSDFG 461
      530 ALTDIVTHTRMNEEQIATVCLSVLKALSYLHNGQVHHRDIKSDSILLTSDGRKILSDFG 589
      462 CAQVSKEVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPNEPPL 521
      590 CAQVSKEVPRKSLVGTPTWMAPEVISRLPYGTEVDIWSLGIWVEMIDGEPYPNEPPL 649
      522 KAMKMRNLNLPRLKNLHKVPSLKGFLDRLVDRPAQATAAELLKHPFLAKAGPPASI 581
      650 QAMRIRDSLPVRKDLHKVSMRLGRFLDMLVREPSQATQAEILLGHGFLKLAGPPSCI 709
      582 VPLMRQNR 589
      710 VPLMRQYR 717

RESULT 10
Q8TB93 ID Q8TB93 PRELIMINARY; PRT; 719 AA.
AC Q8TB93;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE P21(CDKN1A)-activated kinase 7.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024179; AAH24179.1; -.
DR HSSP; P24941; 1BUH.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKBox/RhoGTPase.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00786; pkinase; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS01018; CRIB; 1.
DR PROSITE; PS01017; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

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KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 719 AA; 80794 MW; 536CB5DE65DA9FC3 CRC64;

Query Match 56.0%; Score 1731; DB 4; Length 719;
Best Local Similarity 52.4%; Pred. No. 2.9e-112;
Matches 383; Conservative 66; Mismatches 126; Indels 156; Gaps 17;

QY 1 MFGKKRKEVISAQSNFHRVHTGFDQHEQKFTGLPQWQSLIESARRRPLVDPACIT 60
DB 1 MFGKKKKEIISGPNFHRVHTGFDQEQKFTGLPQWHSLLADTANRPREMDPSCIT 60
QY 61 SIQCAPKTIIVRGSKGAKGALTLLDDEFENMVSRTNSLRDRDPPPPARA-----R 112
DB 61 PIQLAPMKTIIVRGKNPKCKETSINGLLEDNFNISVTRNSLRKESPTPDQCGASSHGPHA 120
QY 113 QENGM-----PEPPATTA-----EGG-----PKKA 132
DB 121 EENGFIPTFSYSSSDTTADYTKYREKSLYGGDLDLPYRGSHAAKONGHVMKMKHGEA 180
QY 133 -----GSRGRFAGH-----SEAG 145
DB 181 YSEVKPLKSFARFADYHSHLDSLSKPESEVSLKWEYQRASSSSPLDYSFQFTPSRTA 240
QY 146 GSGDRRRA-----QP-----EKRPKSREGSGGQESRRDKRPLSGDPVGTTP-QPA 191
DB 241 GTSGCKESLAYSESEWGPSLDDYDRRPKSSYLNTQSPQTMW-QRSRSGSLQEPMPMF 299
QY 192 GLSAGAKLAAGRPNTY-----PRADTDH-----PSRGAQGEHVDVAPNGP 232
DB 300 GASAFKTHPQGHSYNSYTPRLSEPTMCPKVVDYDRAQWVSPPLSGS-----DTYPRGP 354
QY 233 SAGGLAIPOS-----SSSSRPPTRARGA-SPGVLGPHASEPQLAPPACTP----- 278
DB 355 A-----KLPSQSKSGYSSSHQYPSGYHKA-----TLYHHPSLQSSQYISTASYLSL 406
QY 279 AAPAVPGPPRSPQREPORVSHEQFRAALQVLVDGDPGRSYLONFIKIGEGSTGIVCIA 338
DB 407 SSSTVPPSPSGSSSDQPSRVSHQFRAALQVLVSPGDPREYLNFIKIGEGSTGIVCIA 466
QY 339 TVRSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFL 398
DB 467 TEKHTGQVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFL 526
QY 399 EGGALTDIVTHTRMNEEQIAAACLAVLOALSVLHQAQGVHHRDIKSDSILLTHDGRVKLS 458
DB 527 EGGALTDIVTHTRMNEEQIATVCLSVLKALSYLHNGQVHHRDIKSDSILLTSDGRKILSD 586
QY 459 FGCAQVSKEVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPNE 518
DB 587 FGCAQVSKEVPRKSLVGTPTWMAPEVISRLPYGTEVDIWSLGIWVEMIDGEPYPNE 646
QY 519 PPLKAMKMRNLNLPRLKNLHKVPSLKGFLDRLVDRPAQATAAELLKHPFLAKAGPP 578
DB 647 PPLQAMRRIRDSLPVRKDLHKVSMRLGRFLDMLVREPSQATQAEILLGHGFLKLAGPP 706
QY 579 ASIVPLMRQNR 589
DB 707 SCIVPLMRQYR 717

RESULT 11
Q9VXE5 ID Q9VXE5 PRELIMINARY; PRT; 639 AA.
AC Q9VXE5; Q9VYH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG18582 protein (p21 activated kinase related protein).
GN MET OR CG18582.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

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OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.B.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Franknoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis J.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulyov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svarakas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celnik S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RA "Sequencing of *Drosophila melanogaster* genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Masra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochink S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Bertram B., Carlson J.W., Celnik S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Mallowburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RA "Annotation of *Drosophila melanogaster* genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=99035549; PubMed=9811608;
RA Heisenberg M., Raabe T.;
RA "A protein related to p21-activated kinase (PAK) that is involved in
RT neurogenesis in the *Drosophila* adult central nervous system.";
RL Curr. Biol. 8:1223-1226 (1998).
DR EMBL; AE003502; AAF48629.2; -;
DR EMBL; AJ011578; CAA09699.1; -;
DR FlyBase; FBgn0025743; mdt.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/RhoGndg.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Transferase.
SQ SEQUENCE 639 AA; 69620 MW; 414D217F0AEEC1C6 CRC64;
Query Match 48.6%; Score 1501.5; DB 5; Length 639;
Best Local Similarity 50.5%; Pred. No. 2.5e-96;
Matches 336; Conservative 65; Mismatches 158; Indels 107; Gaps 13;
QY 1 MFGKKRKRVEISAPSNFEHRVHTGFDQHEQKFTGLPROMQSL-----IEESARRPKPLVD 55
DB 1 MFSKKKKPLISMPSNEHRVHTGFDKRNKYVGLPLOWASIVGNQILKSNRPLVD 60
QY 56 PACITSIQPGAPKTVR-----GSKGAKDGLTLLDEFENMS----- 93
DB 61 PSEITPTTEILDKTVIRPHNNKADTSLNSSSTMMGSMAPNMAPGAPAHMWSHGP 120
QY 94 -----VTRSNLSRRDSPPPPAR-ARQENGMPEEPATTARGGPKAG-S 134
DB 121 MMMPETGGIVLPKTSHVARSNSLRSSPPRRVRVANVPSPVEEGPAAAGTFCVGGAS 180
QY 135 RGRF-----AGHSEAGGSGDRRRAGPEKPKSREGSGPQESSRDKRPLSG 182
DB 181 SGGFKPPGAHPSLLYNSQAHANGATG-----PLAVRTDTNLQVRSNLAPPSG 230
QY 183 PDVGTTPQAGLASGAKLAAGRPFNTPYPRADTHPSRGAQGEPPHVA NPGPSAGEL--AIP 240
DB 231 GSM--PQQOQTSPVGSVASGTRSN-----HSHTNNGSGSYPPMYP 270
QY 241 QSSSSSSRPPTTRAR--GAPSPGLVGH-----ASEPQLAPACTPAAAPVP 284
DB 271 TSHOQQQQQQQQAQGGQDQONPLJPHAHPHHHHHLAKSASSASSSSGASSAAQOAS 330
QY 285 GPPGPRSPQ-REPQVSHQEFRAALQLVDPGDPSPSYLDNFIKIGEGSTGIVCIATVRSS 343
DB 331 GASGAAGQPKQDQLTHEQFRAALQWVSAGDDPRENLDFHNKIGEGSTGIVCIATDKST 390
QY 344 GKLVAKKMDLRKQORRELLFNEVIMRDYQHENVYMSYLVGDDLWVMELEGAL 403

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Db      391  GRQAVKMDLRKQORRELLFNEVIMRDYHHNPVITYSSFLVNDLWVWVYLEGGAL 450
QY      404  TDIVTHTRMNEEQIAAVCLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCA 463
Db      451  TDIVTHSRMDEQIATVCKQCLKALAYLHSCQVHHRDIKSDSILLAADGRVKLSDFGCA 510
QY      464  QYSKEVPKRKSLVGTPTWMAPELISRLPYGPEVDIWSLGIWVMDGEPVPFNEPPLKA 523
Db      511  QVSQELPKRKLVLGTPYMWSEVIVSRPYGPEVDIWSLGIWVMDGEPFPFNEPPLQA 570
QY      524  MKMIRDNLPPRLKNIHKVSPSLKGFLLVRDPAQRATAAEALLKHPFLAKAGPPASIVP 583
Db      571  MRIRDMQPPNLKNAHKVSPRLQSFLDRMLVEDPAQRATAAEALLAHFLRQAGPSSLVLP 630
QY      584  LMRQNR 589
Db      631  LMRNAR 636

RESULT 12
Q960J8      PRELIMINARY; PRT; 639 AA.
AC Q960J8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LD47563p.
GN MBT OR CG18582.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Friese E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Facleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY052023; AAK93447.1; -.
DR HSSP; P24941; 1BUH.
DR Flybase; FBgn0025743; mbt.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/RhoGndg.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 639 AA; 69592 MW; 2145317F0A8F554 CRC64;

Query Match 48.5%; Score 1497.5; DB 5; Length 639;
Best Local Similarity 50.3%; Pred. No. 4.7e-96;
Matches 335; Conservative 65; Mismatches 159; Indels 107; Gaps 13;

QY      1  MFGKKRKRVRISAPSNPEHRVHTGFDQHEQKFTGLPRQWQL-----IEBSARRPKPLVD 55
Db      1  MFSKKKKKPLISMESNEHRVHTGFDKREKYNVGLPLQWASIVGNQILKSSNRPLPLVD 60

```

```

QY      56  PACITSIQGPAPKTIIVR-----GSKGAKDGAULTLLLDDEFENMS----- 93
Db      61  PSEITPTFILDLTIVRPHNNKADTTLSNSSSTMMGSMAPWNPMPAGAHPMHSHGPG 120
QY      94  -----VTRNSLRDSSPPPAR-AROENGMPEEPATTARGGPGKAG-S 134
Db      121  MMMPETGGIVLPKTSHVARSNSLRSSPPRRVRRVANVPSPVEEGPAAAGTFCVGCGAS 180
QY      135  RGRP-----AGHSEAGGSGDRRAGPEKPKRSREGSGGQESRRDKRPLSG 182
Db      181  SGGFKPGGAHPSLLYNSQAHANGATG-----PLAVRTDQTNLQQTRSNLAPSSG 230
QY      183  PDVGTTPQAGLASGAKLAAGRPFTNTYPRADTHPSRGAQGEPHDVAPNGPSAGGL--AIP 240
Db      231  GSM--PQQQQTSPVGSVASGTRSN-----HSHNTNNGNSGSGYPPMVP 270
QY      241  QSSSSSRPPTRAR--GAPSPGVLGPH-----ASEPQLAPPACTPAAPVP 284
Db      271  TSHQOQQOQQOQAKQGGQDNQNPPLHFAHPPHHQHLAKSASRASSSSGGASAAQAS 330
QY      285  GPPGPRSPQ-REPQVSHHQRAALQVLVDPGDRSYLDNFIKIGEGSTGIVCIATVRSS 343
Db      331  GASGAAGQPKDQDLTHEQFRAALQMVVSAGDPRENLDHFNKIGEGSTGTVCIAIDKST 390
QY      344  GKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMVNSYLVGDELWVWVMEFLEGGAL 403
Db      391  GRQAVKMDLRKQORRELLFNEVIMRDYHHNPVITYSSFLVNDLWVWVYLEGGAL 450
QY      404  TDIVTHTRMNEEQIAAVCLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCA 463
Db      451  TDIVTHSRMDEQIATVCKQCLKALAYLHSCQVHHRDIKSDSILLAADGRVKLSDFGCA 510
QY      464  QYSKEVPKRKSLVGTPTWMAPELISRLPYGPEVDIWSLGIWVMDGEPVPFNEPPLKA 523
Db      511  QVSQELPKRKLVLGTPYMWSEVIVSRPYGPEVDIWSLGIWVMDGEPFPFNEPPLQA 570
QY      524  MKMIRDNLPPRLKNIHKVSPSLKGFLLVRDPAQRATAAEALLKHPFLAKAGPPASIVP 583
Db      571  MRIRDMQPPNLKNAHKVSPRLQSFLDRMLVEDPAQRATAAEALLAHFLRQAGPSSLVLP 630
QY      584  LMRQNR 589
Db      631  LMRNAR 636

RESULT 13
O96372      PRELIMINARY; PRT; 639 AA.
AC O96372;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE STE20 serine/threonine protein kinase homolog.
GN MBT OR CG18582.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Melnick M.B.;
RT "New Drosophila member of the Ste20 serine/threonine kinase family.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031517; AAD01935.1; -.
DR HSSP; P24941; 1BUH.
DR FlyBase; FBgn0025743; mbt.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

```

DT	01-OCT-2002	(TrEMBLrel. 22, Created)
DT	01-OCT-2002	(TrEMBLrel. 22, Last sequence update)
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)
DE	Hypothetical protein FLJ90247.	
OS	Homo sapiens (Human)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxId=9606;	
RP	SEQUENCE FROM N.A.	
RA	Isegai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,	
RA	Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,	
RA	Yamanoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,	
RA	Masuhito Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,	
RA	Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;	
RT	"NEDO human cDNA sequencing project."	
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AK074728; BAC11166.1; -	
DR	GO; GO:0005524; P:ATP binding; IEA.	
DR	GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.	
DR	GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.	
DR	GO; GO:0016740; P:transferase activity; IEA.	
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.	
DR	InterPro; IPR000719; Prot kinase.	
DR	InterPro; IPR002290; Ser Thr pkinase.	
DR	InterPro; IPR001245; Tyr_pkinase.	
DR	pfam; PF00069; pkinase_1	
DR	PRINTS; PR00109; TYRKINASE.	
DR	ProDom; PD000001; Prot kinase; 1.	
DR	SMART; SM00220; S_TKc; 1.	
DR	SMART; SM00219; TyrKc; 1.	
DR	PROSITE; PS50011; PROTEIN KINASE DOM; 1.	
KW	Hypothetical protein; ATP-binding; Transferase.	
QY	SEQUENCE 240 AA; 27332 MW; E3C686288DA913B6 CRC64;	
Query Match 40.23; Score 1241; DB 4; Length 240;		
Best Local Similarity 100.0%; Pred. No. 1e-78;		
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps		
QY	352 MDLRKQQRRELLFNEVVMRDYQHENNVEMNYSVLVGDELWVMELEGALTDIVTHT	
Db	1 MDLRKQQRRELLFNEVVMRDYQHENNVEMNYSVLVGDELWVMELEGALTDIVTHT	
QY	412 MNEEQIAAVCLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPP	
Db	61 MNEEQIAAVCLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPP	
QY	472 RKSLVGTPYMWAPELISRLPYGPEVDIWSLIGIVMIEWDGEPPYNEPPLKAMKMRDN	
Db	121 RKSLVGTPYMWAPELISRLPYGPEVDIWSLIGIVMIEWDGEPPYNEPPLKAMKMRDN	
QY	532 PRLKXNLHKVSPSLKGFLLDRLVDRPAQRATAELLKHPFLAKAGPPASIVFLMRQNT	
Db	181 PRLKXNLHKVSPSLKGFLLDRLVDRPAQRATAELLKHPFLAKAGPPASIVFLMRQNT	
RESULT 15		
Q9CS71	PRELIMINARY;	
ID	Q9CS71	PRT; 229 AA.
AC	Q9CS71;	
DT	01-JUN-2001 (TrEMBLrel. 17, Created)	
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	
DE	5730488L07Rik protein (Fragment).	
DE	5730488L07Rik protein (Fragment).	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxId=10090;	
RP	SEQUENCE FROM N.A.	
RA	STRAIN=C57BL/6J; TISSUE=Embryo;	
RC	MEDLINE=21085660; PubMed=11217851;	

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL; AK017713; BAB30889.1; -.
 DR HSSP; Q63450; IA06.
 DR MGD; MGI:1917834; Pak4.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
 FT NON TER 1
 SQ SEQUENCE 229 AA; 25896 MW; D9CF2CA73CED941E CRC64;

Query Match 37.5%; Score 1160; DB 11; Length 229;
 Best Local Similarity 96.9%; Pred. No. 4.2e-73;
 Matches 222; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 363 LFNEVVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGGALTDIVTHTRMNEEQIAAVCL 422
 Db 1 LFNEVVIMRDYRHENVVEMYSYLVGDELWVWMEFLEGGALTDIVTHTRMNEEQIAAVCL 60
 QY 423 AVLQALSVLHAQGVHHRDKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPLYWM 482
 Db 61 AVLQALAVLHAQGVHHRDKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPLYWM 120
 QY 483 APELISRLPYGPEVDIWSLGIWVIEWVDGPPYFNEPPLKAMQWIRDLNPPRLKNLHKVS 542
 Db 121 APELISRLPYGPEVDIWSLGIWVIEWVDGPPYFNEPPLKAMQWIRDLNPPRLKNLHKAS 180
 QY 543 PSLKGFDLRLVDRDPQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
 Db 181 PSLKGFDLRLVDRDPQRAPAAELLKHPFLTKAGPPASIVPLMRQNRTR 229

Search completed: September 29, 2004, 18:04:41
 Job time : 138.844 secs

B/gnK

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: September 29, 2004, 17:36:56 ; Search time 154.703 Seconds
(without alignments)
1079.395 Million cell updates/sec

Title: US-10-693-367-2
Perfect score: 3090
Sequence: 1 MFGKKRKRVEISAPNSFHR.....LAKAGPPASIVFLMRQNR 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	3090	100.0	591	2	AA55964 Full leng
2	3090	100.0	591	3	AA559128 Human ser
3	3090	100.0	591	7	ADC37307 Nuclear f
4	3090	100.0	591	7	ADD89973 Human can
5	3090	100.0	620	4	ABG19308 Novel hum
6	2558	82.8	501	7	ADC37309 Nuclear f
7	2202.5	71.3	438	7	ADC37305 Nuclear f
8	2073	67.1	398	2	AA55941 Human PAK
9	1734	56.1	719	4	AA38963 Human pol
10	1731	56.0	719	4	AA85705 Novel pro
11	1731	56.0	719	7	ADC37451 Nuclear f
12	1730	56.0	719	4	AAE02187 Human p21
13	1502	48.6	293	7	ADE15851 PAK4KD pr
14	1473.5	47.7	681	2	AA55940 Human PAK
15	1473.5	47.7	681	3	AA803967 Signal tr
16	1473.5	47.7	681	4	AA820337 Human PAK
17	1473.5	47.7	681	5	ABP64709 Human pro
18	1473.5	47.7	701	6	ABU11508 Human MDD
19	1470.5	47.6	681	3	AA803970 Mutant si
20	1470.5	47.6	681	4	AA863230 Amino aci
21	1448.5	46.9	681	3	AA803971 Mutant si
22	1335.5	43.2	641	5	AAE16269 Human kin
23	1277	41.3	250	3	AA559129 Human PAK
24	1251.5	40.5	632	4	AA85788 Human kin
25	1244.5	40.3	547	4	AA867825 Human P21

26	1241	40.2	240	4	AAW93297	AAm93297 Human pol
27	1241	40.2	240	7	ADC37303	Adc37303 Nuclear f
28	1164.5	37.7	250	8	ADE28303	Ade28303 Human KPP
29	1029	33.3	311	4	AAE20336	AAe20336 Human PAK
30	955.5	30.9	575	4	ABB60665	Abb60665 Drosophil
31	937.5	30.3	704	4	ABB66726	Abb66726 Drosophil
32	937.5	30.3	704	4	ABB64989	Abb64989 Drosophil
33	909	29.4	544	2	AAW72757	AAw72757 Human dou
34	908	29.4	544	6	AAE14906	AAe14906 Human P21
35	907	29.4	544	2	AA55960	AAy55960 Mouse STE
36	907	29.4	544	5	ABB57290	Abb57290 Mouse isc
37	904	29.3	524	5	AAO15488	AAo15488 Human ser
38	900.5	29.1	390	4	ABG19309	Abg19309 Novel hum
39	900	29.1	524	2	AAW95521	AAw95521 Protease
40	900	29.1	524	5	AAO22775	AAo22775 Rabbit pr
41	899	29.1	520	2	AAW15265	AAw15265 Rat beta-
42	895.5	29.0	525	3	AA803969	AAo3969 p-21 acti
43	895.5	29.0	525	6	AAO26548	AAo26548 Human PAK
44	895.5	29.0	525	6	ABR59699	ABr59699 Human p21
45	895.5	29.0	525	6	ABR63659	ABr63659 Human p21

ALIGNMENTS

RESULT 1
AA55964
ID AA55964 standard; protein; 591 AA.

XX
AC
AA55964;

XX
AC
18-FEB-2000 (first entry)

XX
DE
Full length human PAK5 protein.

XX
KW
Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic;
antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;
neuroprotective; cardiant; cerebrotective; cytostatic; antidiabetic;
vulnery; STE20; protein kinase; SILK2; SILK3; SILK4; SILK5; SILK6; SILK7;
ZC1; ZC2; ZC3; ZC4; KHS2; SULU3; GSK2; PAK4; PAK5; antagonist;
antibody; gene therapy; rheumatoid arthritis; atherosclerosis; asthma;
inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
myocardial infarction; cardiovascular disease; stroke; renal failure;
oxidative stress-related neurodegenerative disorder; Parkinson's disease;
amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
mesangial disorder; growth regulation; wound healing; T cell activation;
immunosuppressant.

XX
OS
Homo sapiens.

XX
PN
MO9953036-A2.

XX
PD
21-OCT-1999.

XX
PF
13-APR-1999; 99WO-US008150.

XX
PR
14-APR-1998; 98US-0081784P.

XX
PA
(SUGS-) SUGEN INC.

XX
PI
Plowman G, Martinez R, Whyte D;

XX
DR
WPI; 1999-611301/52.

XX
DR
N-PSDB; AA240538.

XX
PT
Novel kinase-related polypeptides used for the diagnosis and treatment of

XX
PT
kinase-related diseases and disorders.

XX
PS
Claim 11; Page 366-368; 387pp; English.

XX
CC
This sequence represents a novel STE20-related protein kinase. The

CC invention relates to nucleic acid molecule encoding a kinase polypeptide
 CC selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3,
 CC ZC4, XHS2, SULU1, SULU3, GSK2, PAK4 and PAK5. The proteins are used to
 CC identify agonists and antagonists, and to raise antibodies. The
 CC polynucleotides are useful in gene therapy protocols. The polynucleotides,
 CC polypeptides, antibodies, antagonists and agonists may be used to treat
 CC diseases such as immune-related disorders and diseases (e.g. rheumatoid
 CC arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g.
 CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
 CC rhinitis, autoimmunity, and organ transplantation, chronic inflammatory
 CC pelvic disease, multiple sclerosis, organ transplantation, myocardial
 CC infarction, cardiovascular disease, stroke, renal failure, oxidative
 CC stress-related neurodegenerative disorders (e.g. amyotrophic lateral
 CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,
 CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
 CC mellitus, fibrotic and mesangial disorders. The proteins may also be
 CC useful for cell growth regulation (e.g. in wound healing), T cell
 CC activation, mitosis control, and as immunosuppressants
 XX
 SQ Sequence 591 AA;

Query Match 100.0%; Score 3090; DB 2; Length 591;
 Best Local Similarity 100.0%; Pred. No. 2.3e-216; Mismatches 0; Indels 0; Gaps 0;
 Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFGKKKRVETISAPNFEHVRHTGFDQHEQKFTGLPROMQSLIESARRPKPLVDPACIT 60
 DB 1 MFGKKKRVETISAPNFEHVRHTGFDQHEQKFTGLPROMQSLIESARRPKPLVDPACIT 60
 QY 61 SIQGPAPKTIIVRSGKADGALTLLDEFNNMVSRTNSLRDSDPPPPARARQENMPPE 120
 DB 61 SIQGPAPKTIIVRSGKADGALTLLDEFNNMVSRTNSLRDSDPPPPARARQENMPPE 120
 QY 121 PATTARGGPKAGSGRAGHSEAGGSDRRRAGPEKPKSRREGSGGPQSSRDKRL 180
 DB 121 PATTARGGPKAGSGRAGHSEAGGSDRRRAGPEKPKSRREGSGGPQSSRDKRL 180
 QY 181 SGPDVGTTPQAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEHVDVAPNGFSAGGLAIP 240
 DB 181 SGPDVGTTPQAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEHVDVAPNGFSAGGLAIP 240
 QY 241 QSSSSSSRPPTARGAPSPGLGPHASEPQLAPPACTPAAPVPGPPGPRSPQRPQVS 300
 DB 241 QSSSSSSRPPTARGAPSPGLGPHASEPQLAPPACTPAAPVPGPPGPRSPQRPQVS 300
 QY 301 HEQFRAALQLVVDGPRSYLDFNFIKIGEGSTGIVCIATVRSGLVAVKMDLRKQRR 360
 DB 301 HEQFRAALQLVVDGPRSYLDFNFIKIGEGSTGIVCIATVRSGLVAVKMDLRKQRR 360
 QY 361 ELLFNEVIMRDYQHENVVEMYSYLVGDELVMWMEFLEGGALTIDIVTHRNNEEQIAAV 420
 DB 361 ELLFNEVIMRDYQHENVVEMYSYLVGDELVMWMEFLEGGALTIDIVTHRNNEEQIAAV 420
 QY 421 CLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPT 480
 DB 421 CLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPT 480
 QY 481 WMAPELISRLPYGPEVDIWSLGIWVEMVDGPPYFNEPPLKAMKIRNLPRLKNLHK 540
 DB 481 WMAPELISRLPYGPEVDIWSLGIWVEMVDGPPYFNEPPLKAMKIRNLPRLKNLHK 540
 QY 541 VSPSLKGLFDRLLVRDPAQATAAELLKHFPFLAKAGPPASIVPLMRQNRTR 591
 DB 541 VSPSLKGLFDRLLVRDPAQATAAELLKHFPFLAKAGPPASIVPLMRQNRTR 591

RESULT 2

AA59128

ID AA59128 standard; protein; 591 AA.

XX

AC AA59128;

XX

DT 08-MAR-2000 (first entry)

XX Human serine/threonine kinase, PAK4.
 DE
 XX PAK4; serine/threonine kinase; GTPase; intracellular signal cascade; Rac;
 XX Cdc42H; morphogenesis; mitogenesis; JNK; p38 MAP kinase; human;
 KW actin polymerization; filopodia; cancer; arthritis.
 XX
 OS Homo sapiens.
 XX
 XX WO9963073-A1.
 PN
 XX 09-DEC-1999.
 PD
 XX 21-MAY-1999; 99WO-US011341.
 PF
 XX 21-MAY-1999; 98US-00082737.
 PR
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 PA
 XX Minden A;
 PI
 XX
 XX WPI: 2000-072881/06.
 DR
 XX N-PSDB; AA240857.
 DR
 XX Novel mammalian nucleic acid useful for treating cancer and arthritis.
 PT
 XX Claim 8; Fig 1A-B; 95pp; English.
 PS
 XX The invention relates to an isolated mammalian nucleic acid that encodes
 CC PAK4, a novel serine/threonine kinase or its mutant homolog. PAK4 is an
 CC effector for the GTPases Rac and Cdc42Hs which are involved in
 CC intracellular signal cascades, morphogenesis and mitogenesis, and
 CC activate the JNK and p38 MAP kinase pathways. Inhibiting interaction of
 CC PAK4 with these enzymes will thus result in inhibition of actin
 CC polymerization and formation of filopodia. The PAK4 nucleic acid used for
 CC recombinant production of the protein, and as a source of probes for
 CC identifying homologous sequences and of (anti)sense oligonucleotides for
 CC inhibiting PAK4 expression. The protein, or its fragments, are used to
 CC raise specific antibodies and these are useful as ligands for therapeutic
 CC inhibition of interaction between PAK4 and its native binding partners.
 CC Inhibition of PAK4 activity or expression is used for treatment of cancer
 CC and arthritis. The present sequence represents the human serine/threonine
 CC kinase, PAK4
 CC
 XX Sequence 591 AA;

Query Match 100.0%; Score 3090; DB 3; Length 591;
 Best Local Similarity 100.0%; Pred. No. 2.3e-216; Mismatches 0; Indels 0; Gaps 0;
 Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFGKKKRVETISAPNFEHVRHTGFDQHEQKFTGLPROMQSLIESARRPKPLVDPACIT 60
 DB 1 MFGKKKRVETISAPNFEHVRHTGFDQHEQKFTGLPROMQSLIESARRPKPLVDPACIT 60
 QY 61 SIQGPAPKTIIVRSGKADGALTLLDEFNNMVSRTNSLRDSDPPPPARARQENMPPE 120
 DB 61 SIQGPAPKTIIVRSGKADGALTLLDEFNNMVSRTNSLRDSDPPPPARARQENMPPE 120
 QY 121 PATTARGGPKAGSGRAGHSEAGGSDRRRAGPEKPKSRREGSGGPQSSRDKRL 180
 DB 121 PATTARGGPKAGSGRAGHSEAGGSDRRRAGPEKPKSRREGSGGPQSSRDKRL 180
 QY 181 SGPDVGTTPQAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEHVDVAPNGFSAGGLAIP 240
 DB 181 SGPDVGTTPQAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEHVDVAPNGFSAGGLAIP 240
 QY 241 QSSSSSSRPPTARGAPSPGLGPHASEPQLAPPACTPAAPVPGPPGPRSPQRPQVS 300
 DB 241 QSSSSSSRPPTARGAPSPGLGPHASEPQLAPPACTPAAPVPGPPGPRSPQRPQVS 300
 QY 301 HEQFRAALQLVVDGPRSYLDFNFIKIGEGSTGIVCIATVRSGLVAVKMDLRKQRR 360
 DB 301 HEQFRAALQLVVDGPRSYLDFNFIKIGEGSTGIVCIATVRSGLVAVKMDLRKQRR 360

QY 361 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGALTIDIVTHRMNEEQIAAV 420
 Db 361 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGALTIDIVTHRMNEEQIAAV 420
 QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGFCQAQVSKEVPRRKSILVGTPT 480
 Db 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGFCQAQVSKEVPRRKSILVGTPT 480
 QY 481 WMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPNEPPLKAMKMIKMDLPPRLKNLHK 540
 Db 481 WMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPNEPPLKAMKMIKMDLPPRLKNLHK 540
 QY 541 VPSLKGFLDRLVLRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
 Db 541 VPSLKGFLDRLVLRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
 RESULT 3
 ADC37307
 ID ADC37307 standard; protein; 591 AA.
 XX
 AC ADC37307;
 DT 18-DEC-2003 (first entry)
 XX
 DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 140.
 XX
 KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
 KW cancer; infectious disease; bone disease; AIDS;
 KW neurodegenerative disease; ischaemic disorder; Antiinflammatory;
 KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
 KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003048202-A2.
 XX
 PD 12-JUN-2003.
 XX
 PF 03-DEC-2002; 2002WO-JP012644.
 XX
 PR 03-DEC-2001; 2001JP-00368692.
 PR 05-DEC-2001; 2001US-0335829P.
 PR 03-OCT-2002; 2002JP-00291302.
 PR 04-OCT-2002; 2002US-0415769P.
 XX
 PA (ASAH) ASahi KASEI KK.
 XX
 PI Matsuda A, Muramatsu S;
 XX
 DR WPI: 2003-505282/47.
 DR N-PSDB; ADC37306.
 XX
 PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
 PT useful for treating inflammation, autoimmune diseases, cancers,
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
 PT ischemic disorders.
 XX
 PS Claim 1; SEQ ID NO 140; 938pp; English.
 XX
 CC The present invention relates to novel proteins and their coding
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
 CC kappaB). The proteins and their coding sequences are useful for treating
 CC a disease associated with NF-kappaB activation, such as inflammation,
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
 CC neurodegenerative diseases, or ischaemic disorders.
 XX
 SQ Sequence 591 AA;
 Query Match 100.0%; Score 3090; DB 7; Length 591;
 Best Local Similarity 100.0%; Pred. No. 2.3e-216;
 Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKRRKRVVEISAPSNFEHRVHTGPDQHEQKFTGLPRQWOSLIEESARBPKLVDPAKIT 60
 Db 1 MEKRRKRVVEISAPSNFEHRVHTGPDQHEQKFTGLPRQWOSLIEESARBPKLVDPAKIT 60
 QY 61 STQPGAPKTIIVRSGKAKDGALTLLDDEFENSVTRSNLSRRDSPPPPARARQENGWPEE 120
 Db 61 STQPGAPKTIIVRSGKAKDGALTLLDDEFENSVTRSNLSRRDSPPPPARARQENGWPEE 120
 QY 121 PATTARGGKAGSRORFAGHSEAGGSGDRRRRAGPEKPKSRREGSGGFQSSSRDKRPL 180
 Db 121 PATTARGGKAGSRORFAGHSEAGGSGDRRRRAGPEKPKSRREGSGGFQSSSRDKRPL 180
 QY 181 SGPDVCTTPOAGLASAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVAPNGPSAGGLAIP 240
 Db 181 SGPDVCTTPOAGLASAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVAPNGPSAGGLAIP 240
 QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPQLAPPACTPAAPAVPPGPPRSPOREPORVS 300
 Db 241 QSSSSSRPPTRARGAPSPGVLGPHASEPQLAPPACTPAAPAVPPGPPRSPOREPORVS 300
 QY 301 HEQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCIATVRSGLVAVKXMDLRKQRR 360
 Db 301 HEQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCIATVRSGLVAVKXMDLRKQRR 360
 QY 361 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGALTIDIVTHRMNEEQIAAV 420
 Db 361 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGALTIDIVTHRMNEEQIAAV 420
 QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGFCQAQVSKEVPRRKSILVGTPT 480
 Db 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGFCQAQVSKEVPRRKSILVGTPT 480
 QY 481 WMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPNEPPLKAMKMIKMDLPPRLKNLHK 540
 Db 481 WMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPNEPPLKAMKMIKMDLPPRLKNLHK 540
 QY 541 VPSLKGFLDRLVLRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
 Db 541 VPSLKGFLDRLVLRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
 RESULT 4
 ADD89973
 ID ADD89973 standard; protein; 591 AA.
 XX
 AC ADD89973;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human cancer-associated protein kinase PAK4.
 XX
 KW PAK4; protein kinase; enzyme; cancer; cytostatic; immunosuppressive;
 KW antidiabetic; antirheumatic; antiarthritic; antipsoriatic;
 KW antiangiogenic; antiarteriosclerotic; antiinflammatory; vulnery;
 KW gynaecological; neuroprotective; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003083096-A2.
 XX
 PD 09-OCT-2003.
 XX
 PF 21-MAR-2003; 2003WO-CA000409.
 XX
 PR 28-MAR-2002; 2002US-0368853P.
 XX
 PA (KINE-) KINETEK PHARM INC.
 XX
 PI Delaney AD;
 XX
 DR WPI; 2003-833542/77.
 DR N-PSDB; ADD89972.

XX New nucleic acids encoding cancer associated protein kinases, useful as
PT targets for screening pharmaceutical agents that inhibit the growth of
PT tumor cells, or for diagnosing and treating cancer, inflammation or
PT autoimmune disease.

XX Claim 1; Page 77-78; 91pp; English.

XX The present sequence is the protein sequence of human cancer-associated
CC protein kinase, PAK4. PAK-related kinase PAK4 is an effector molecule for
CC Cdc42Hs. Its gene expression is up-regulated in cancers of the brain,
CC lung, muscle and uterus. PAK4 is one of a set of protein kinases that are
CC shown by the invention to be over-expressed in hyper-proliferative cells.
CC These protein kinases provide targets for drug screening for agents
CC effective in inhibiting the growth or metastasis of tumour cells, and for
CC determining other molecular targets in kinase signal transduction
CC pathways involved in transformation and growth of tumour cells. A claimed
CC method for inhibiting the growth of a cancer cell involves down-
CC regulating the activity of the protein kinase using an antisense sequence
CC or inhibitor of kinase activity, especially where the cancer cell is a
CC breast, liver, colon, muscle, prostate, kidney, lung, placental or
CC uterine cancer cell. Detection of over-expression in cancers provides a
CC useful diagnostic for predicting patient prognosis and probability of
CC drug effectiveness. Agents that specifically bind the protein kinases can
CC be used for treatment and visualisation of tumours in patients. The
CC protein kinase polypeptides and nucleic acids may also be used for
CC treating hyperproliferative diseases, such as autoimmune disease,
CC diabetes mellitus, multiple sclerosis, rheumatoid arthritis, psoriasis,
CC atherosclerosis, inflammation, scarring, endometriosis and angiogenesis.

XX Sequence 591 AA;

Query Match 100.0%; Score 3090; DB 7; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.3e-216; Indels 0; Gaps 0;
Matches 591; Conservative 0; Mismatches 0;

QY 1 MFGKKRKRVEISAPSNFHRVHTGPDQHEQKFTGLPRQWQSLIESARRPKPLVDPAKIT 60
Db 1 MFGKKRKRVEISAPSNFHRVHTGPDQHEQKFTGLPRQWQSLIESARRPKPLVDPAKIT 60
QY 61 SIQPGAPKTVIRGSKAKGALGTLTLLDEFENMSVTRNSLRDSDPPPPARARQENMPPE 120
Db 61 SIQPGAPKTVIRGSKAKGALGTLTLLDEFENMSVTRNSLRDSDPPPPARARQENMPPE 120
QY 121 PATTARGGPKAGSRGFAHSGAGGSDRRRAGPEKPKSRREGSGGPGQSSRRDKRPL 180
Db 121 PATTARGGPKAGSRGFAHSGAGGSDRRRAGPEKPKSRREGSGGPGQSSRRDKRPL 180
QY 181 SGPDVGTPOAGLASGAKLAAGRPFNTYPRADTHPSRGAQGEPHDVAENGPSAGGLAIP 240
Db 181 SGPDVGTPOAGLASGAKLAAGRPFNTYPRADTHPSRGAQGEPHDVAENGPSAGGLAIP 240
QY 241 QSSSSSRPPTARGAPSGVLGPHASEPOLAPACTPAAPVGPGRSPQREPORVS 300
Db 241 QSSSSSRPPTARGAPSGVLGPHASEPOLAPACTPAAPVGPGRSPQREPORVS 300
QY 301 HQQFRAALQVLDGPRSYLDNFIKIGRGSTGIVCIATVRSGLKLVAVKMDLRKQRR 360
Db 301 HQQFRAALQVLDGPRSYLDNFIKIGRGSTGIVCIATVRSGLKLVAVKMDLRKQRR 360
QY 361 ELLFNEWIMRDYQHENVVMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 420
Db 361 ELLFNEWIMRDYQHENVVMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 420
QY 421 CLAVLOALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPY 480
Db 421 CLAVLOALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPY 480
QY 481 WNAPELISRLPYGPEVDINSLGIMVEMVDGEPYFNEPPLKAMKIMRDNLPRLKNLHK 540
Db 481 WNAPELISRLPYGPEVDINSLGIMVEMVDGEPYFNEPPLKAMKIMRDNLPRLKNLHK 540
QY 541 VPSLKGFLDRLLRVDPQAQRATAELLKHFFLAKAGPPASIVPLMRQNRT 591

Db 541 VPSLKGFLDRLLRVDPQAQRATAELLKHFFLAKAGPPASIVPLMRQNRT 591

RESULT 5
ABG19308

ID ABG19308 standard; protein; 620 AA.

XX AC ABG19308;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #19299.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX XX 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS83495.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX PS Claim 20; SEQ ID NO 49667; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
sequences. (I) is useful as hybridisation probes, polymerase chain
reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
and in recombinant production of (II). The polynucleotides are also used
in diagnostics as expressed sequence tags for identifying expressed
genes. (I) is useful in gene therapy techniques to restore normal
activity of (II) or to treat disease states involving (II). (II) is
useful for generating antibodies against it, detecting or quantitating a
polypeptide in tissue, as molecular weight markers and as a food
supplement. (II) and its binding partners are useful in medical imaging
of sites expressing (II). (I) and (II) are useful for treating disorders
involving aberrant protein expression or biological activity. The
polypeptide and polynucleotide sequences have application in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits to assess biodiversity
and to produce other types of data and products dependent on DNA and
amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
amino acid sequences of the invention. Note: The sequence data for this
patent did not appear in the printed specification, but was obtained in
electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 620 AA;

Query Match 100.0%; Score 3090; DB 4; Length 620;

Best Local Similarity 100.0%; Pred. No. 2.5e-216;

Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGKKRKRVEISAPSNFHRVHTGPDQHEQKFTGLPRQWQSLIESARRPKPLVDPAKIT 60

Db 30 MFGKKRKRVEISAPSNFHRVHTGPDQHEQKFTGLPRQWQSLIESARRPKPLVDPAKIT 89

QY 61 SIQGAPKTIVRGSKGAKDQALTLTLLDEPNMVSITRSNLSLRDSSPPPPAPARQENGMPPEE 120
 DB 90 SIQGAPKTIVRGSKGAKDQALTLTLLDEPNMVSITRSNLSLRDSSPPPPAPARQENGMPPEE 149
 QY 121 PATTARGGPGKAGSRGRFAGHSAGGSGDRRRAGPEKRPKSSREGSGGQESSRDKRPL 180
 DB 150 PATTARGGPGKAGSRGRFAGHSAGGSGDRRRAGPEKRPKSSREGSGGQESSRDKRPL 209
 QY 181 SGPDVCTPQAGLASAKLAAGHPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
 DB 210 SGPDVCTPQAGLASAKLAAGHPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 269
 QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPRSPQREPORVS 300
 DB 270 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPRSPQREPORVS 329
 QY 301 HEQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORR 360
 DB 330 HEQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORR 389
 QY 361 ELLFNEVIMRDYQHENVVEMYNYSYLVGDELWVMEFLEGALTDIVTHTRMNEEQIAAV 420
 DB 390 ELLFNEVIMRDYQHENVVEMYNYSYLVGDELWVMEFLEGALTDIVTHTRMNEEQIAAV 449
 QY 421 CLAVLQALSVLHAQGVITHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSILVGTTPY 480
 DB 450 CLAVLQALSVLHAQGVITHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSILVGTTPY 509
 QY 481 WMAPELISRLPYGPEVDIWSLGIWMIEMVDGEPYFNEPPLKAMKIMRDLNLPRLKNLHK 540
 DB 510 WMAPELISRLPYGPEVDIWSLGIWMIEMVDGEPYFNEPPLKAMKIMRDLNLPRLKNLHK 569
 QY 541 VPSLKGFLDRLLRDPAQRATAAELLKHPFLAKAGPPASIVPLMQNRTR 591
 DB 570 VPSLKGFLDRLLRDPAQRATAAELLKHPFLAKAGPPASIVPLMQNRTR 620

RESULT 6

ADC37309
 ID ADC37309 standard; protein; 501 AA.
 XX ADC37309;
 AC
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 142.
 XX
 KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
 KW cancer; infectious disease; bone disease; AIDS;
 KW neurodegenerative disease; ischaemic disorder; Antiinflammatory;
 KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
 KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003048202-A2.
 XX
 PD 12-JUN-2003.
 XX
 PF 03-DEC-2002; 2002WO-JP012644.
 XX
 PR 03-DEC-2001; 2001JP-00368692.
 PR 05-DEC-2001; 2001US-0335829P.
 PR 03-OCT-2002; 2002JP-00291302.
 PR 04-OCT-2002; 2002US-0415769P.
 XX
 PA (ASAH) ASahi KASEI KK.
 XX
 XX Matsuda A, Muramatsu S;
 PI
 XX WPI; 2003-505282/47.
 DR N-PSDB; ADC37308.
 DR

XX
 PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
 PT useful for treating inflammation, autoimmune diseases, cancers,
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
 PT ischemic disorders.
 XX
 PS Claim 1; SEQ ID NO 142; 938pp; English.
 XX
 CC The present invention relates to novel proteins and their coding
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
 CC kappaB). The proteins and their coding sequences are useful for treating
 CC a disease associated with NF-kappaB activation, such as inflammation,
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
 CC neurodegenerative diseases, or ischaemic disorders.
 XX
 SQ Sequence 501 AA;

Query Match 82.8%; Score 2558; DB 7; Length 501;
 Best Local Similarity 84.8%; Pred. No. 1e-177;
 Matches 501; Conservative 0; Mismatches 0; Indels 90; Gaps 1;
 QY 1 MFGRKRVVEISAPSNFEHRVHTGPDQHQKFTGLPRQWQSLIEESARRPKPLVDPAKIT 60
 DB 1 MFGRKRVVEISAPSNFEHRVHTGPDQHQKFTGLPRQWQSLIEESARRPKPLVDPAKIT 60
 QY 61 SIQGAPKTIVRGSKGAKDQALTLTLLDEPNMVSITRSNLSLRDSSPPPPAPARQENGMPPEE 120
 DB 61 SIQGAPKTIVRGSKGAKDQALTLTLLDEPNMVSITRSNLSLRDSSPPPPAPARQENGMPPEE 120
 QY 121 PATTARGGPGKAGSRGRFAGHSAGGSGDRRRAGPEKRPKSSREGSGGQESSRDKRPL 180
 DB 121 PATTARGGPGK----- 131
 QY 181 SGPDVCTPQAGLASAKLAAGHPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
 DB 132 -----GEPHDVAPNGPSAGGLAIP 150
 QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPRSPQREPORVS 300
 DB 151 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPRSPQREPORVS 210
 QY 301 HEQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORR 360
 DB 211 HEQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORR 270
 QY 361 ELLFNEVIMRDYQHENVVEMYNYSYLVGDELWVMEFLEGALTDIVTHTRMNEEQIAAV 420
 DB 271 ELLFNEVIMRDYQHENVVEMYNYSYLVGDELWVMEFLEGALTDIVTHTRMNEEQIAAV 330
 QY 421 CLAVLQALSVLHAQGVITHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSILVGTTPY 480
 DB 331 CLAVLQALSVLHAQGVITHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSILVGTTPY 390
 QY 481 WMAPELISRLPYGPEVDIWSLGIWMIEMVDGEPYFNEPPLKAMKIMRDLNLPRLKNLHK 540
 DB 391 WMAPELISRLPYGPEVDIWSLGIWMIEMVDGEPYFNEPPLKAMKIMRDLNLPRLKNLHK 450
 QY 541 VPSLKGFLDRLLRDPAQRATAAELLKHPFLAKAGPPASIVPLMQNRTR 591
 DB 451 VPSLKGFLDRLLRDPAQRATAAELLKHPFLAKAGPPASIVPLMQNRTR 501

RESULT 7

ADC37305
 ID ADC37305 standard; protein; 438 AA.
 XX
 AC ADC37305;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 138.
 XX
 KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
 KW

cancer; infectious disease; bone disease; AIDS;
 neurodegenerative disease; ischaemic disorder; Antinflammatory;
 Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
 Neuroprotective; Nootropic; Cardiant; Gene therapy; human.
 Homo sapiens.
 WO2003048202-A2.
 12-JUN-2003.
 03-DEC-2002; 2002WO-JP012644.
 03-DEC-2001; 2001JP-00368692.
 05-DEC-2001; 2001US-0335829P.
 03-OCT-2002; 2002JP-00291302.
 04-OCT-2002; 2002US-04115769P.
 (ASAH) ASahi KASEI KK.
 Matsuda A, Muramatsu S;
 WPI; 2003-505282/47.
 N-PSDB; ADC37304.
 New purified protein that activates nuclear kappa B (NF-kappaB),
 useful for treating inflammation, autoimmune diseases, cancers,
 infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
 ischemic disorders.
 Claim 1; SEQ ID NO 138; 938pp; English.
 The present invention relates to novel proteins and their coding
 sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
 kappaB). The proteins and their coding sequences are useful for treating
 a disease associated with NF-kappaB activation, such as inflammation,
 autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
 neurodegenerative diseases, or ischaemic disorders.
 SQ Sequence 438 AA;
 Query Match 71.3%; Score 2202.5; DB 7; Length 438;
 Best Local Similarity 74.1%; Pred. No. 6.5e-152;
 Matches 438; Conservative 0; Mismatches 0; Indels 153; Gaps 1;
 1 MFGKRRVEISAPSNFHRVHTGFDQHEQKFTGLPRQWQSLIESARRPKPLVDPACT 60
 1 MFGKRRVEISAPSNFHRVHTGFDQHEQKFTGLPRQWQSLIESARRPKPLVDPACT 60
 61 SIQPGAPKTVIRGSKGAKGALTLILDEFENMSVTRSLRSDPPPPARARQGMPEE 120
 61 SIQPGAPK-----68
 121 PATTARGGKAGSRGRFAGHSEAGGSGDRRRAGPEKPKSRREGSGPQESSRDKRPL 180
 69 -----68
 181 SGPDVGTQPAGLASKALAGRPNTYPRADTHPSRGAQGEHDVAPNGPSAGGLAIP 240
 69 -----GEPHDVAPNGPSAGGLAIP 87
 241 QSSSSSRPPTTRAGAPSGVLGPHASEPQLAPPACTPAAPVPGPPGPRSPQRPQVS 300
 88 QSSSSSRPPTTRAGAPSGVLGPHASEPQLAPPACTPAAPVPGPPGPRSPQRPQVS 147
 301 HQFRAALQVDPGPRSLDNFIKIGESTGIVCIATVRSGLVAVKMDLRKQOR 360
 148 HQFRAALQVDPGPRSLDNFIKIGESTGIVCIATVRSGLVAVKMDLRKQOR 207
 361 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGALTDIVTHTRNNEEQIAAV 420
 208 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGALTDIVTHTRNNEEQIAAV 267

QY 421 CLAVLQALSVLHAQGVIIHRDIKSDSILLTHDGRVKLSDFGFCQAQSVKVPKRKSLVGTPT 480
 Db 268 CLAVLQALSVLHAQGVIIHRDIKSDSILLTHDGRVKLSDFGFCQAQSVKVPKRKSLVGTPT 327
 QY 481 WMAPELISRLPYGPEVDIWSLGIWVEMVDGEPPEPPFLKAMKMDIRNLPRLKLNHK 540
 Db 328 WMAPELISRLPYGPEVDIWSLGIWVEMVDGEPPEPPFLKAMKMDIRNLPRLKLNHK 387
 QY 541 VSPSLKGFGLDRLVDRDPAQRATAELLKHPFLAKAGPPASIVPLMRQNRTR 591
 Db 388 VSPSLKGFGLDRLVDRDPAQRATAELLKHPFLAKAGPPASIVPLMRQNRTR 438
 RESULT 8
 AAY55941
 ID AAY55941 standard; protein; 398 AA.
 XX AAY55941;
 DT 18-FEB-2000 (first entry)
 XX Human PAK5 protein.
 DE
 XX Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic;
 KW Antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;
 KW neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;
 KW vulnery; STE20; protein kinase; STLK2; STLK3; STLK4; STLK5; STLK6; STLK7;
 KW ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GEK2; PAK4; PAK5; antagonist;
 KW antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
 KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
 KW rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
 KW myocardial infarction; cardiovascular disease; stroke; renal failure;
 KW amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
 KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
 KW mesangial disorder; growth regulation; wound healing; T cell activation;
 KW immunosuppressant.
 XX
 OS Homo sapiens.
 XX
 PN WO9953036-A2.
 XX
 PD 21-OCT-1999.
 XX
 PF 13-APR-1999; 99WO-US008150.
 XX
 PR 14-APR-1998; 98US-0081784P.
 XX
 PA (SUGE-) SUGEN INC.
 PI Plowman G, Martinez R, Whyte D;
 XX
 DR WPI: 1999-611301/52.
 DR N-PSDB; AA240493.
 XX
 PT Novel kinase-related polypeptides used for the diagnosis and treatment of
 PT kinase-related diseases and disorders.
 PS Disclosure; Page 310-312; 387pp; English.
 XX
 CC This sequence represents a novel STE20-related protein kinase. The
 CC invention relates to nucleic acid molecule encoding a kinase polypeptide
 CC selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3,
 CC ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to
 CC identify agonists and antagonists, and to raise antibodies. The
 CC polynucleotides are useful in gene therapy protocols. The polynucleotides,
 CC polypeptides, antibodies, antagonists and agonists may be used to treat
 CC diseases such as immune-related disorders and diseases (e.g. rheumatoid
 CC arthritis, artherosclerosis, chronic inflammatory bowel disease (e.g.
 CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
 CC rhinitis, autoimmunity, and organ transplantation, chronic inflammatory
 CC pelvic disease, multiple sclerosis, organ transplantation, myocardial
 CC infarction, cardiovascular disease, stroke, renal failure, oxidative

CC stress-related neurodegenerative disorders (e.g. amyotrophic lateral
CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,
CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
CC mellitus, fibrotic and mesangial disorders. The proteins may also be
CC useful for cell growth regulation (e.g. in wound healing), T cell
CC activation, mitosis control, and as immunosuppressants
XX
SQ Sequence 398 AA;

Query Match 67.1%; Score 2073; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 1.5e-142;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 ASGAKLAAGRPNTYPRADTDHPSRGAQGEHPHVPNGSPAGGLAIPQSSSSSRPPTRA 253
Db 1 ASGAKLAAGRPNTYPRADTDHPSRGAQGEHPHVPNGSPAGGLAIPQSSSSSRPPTRA 60

QY 254 RGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGPRSPQEPQVSHQFRAALQLVVD 313
Db 61 RGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGPRSPQEPQVSHQFRAALQLVVD 120

QY 314 PGDPRSYLDFIKIGSGTIVCIATVRSGLKLVAVKMDLRKQORRELLFNEVIMRDY 373
Db 121 PGDPRSYLDFIKIGSGTIVCIATVRSGLKLVAVKMDLRKQORRELLFNEVIMRDY 180

QY 374 QHENVVEMYSYLVGDELWVMEFLGEGALTDIVTHRMNEEQIAAVCLAVLQALSVLHA 433
Db 181 QHENVVEMYSYLVGDELWVMEFLGEGALTDIVTHRMNEEQIAAVCLAVLQALSVLHA 240

QY 434 QGVHRIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSILVGTVPWMAPELISRLPYG 493
Db 241 QGVHRIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSILVGTVPWMAPELISRLPYG 300

QY 494 PEVDIWSLGMTVEMVDGEPPEYNEPPLKAMKIRNLPRLKNLKVSPSLKGFLLRL 553
Db 301 PEVDIWSLGMTVEMVDGEPPEYNEPPLKAMKIRNLPRLKNLKVSPSLKGFLLRL 360

QY 554 VRDPAQRATAAEILLKHPFLKAGPPASIVPLMRQNRTR 591
Db 361 VRDPAQRATAAEILLKHPFLKAGPPASIVPLMRQNRTR 398

RESULT 9
AAM38963
ID AAM38963 standard; protein; 719 AA.
XX
AC AAM38963;
XX
DT 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 2108.
XX
KW Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 28-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI58119.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 3; SEQ ID NO 2108; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with neurotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 719 AA;

Query Match 56.1%; Score 1734; DB 4; Length 719;
Best Local Similarity 52.7%; Pred. No. 1.5e-117;
Matches 385; Conservative 64; Mismatches 126; Indels 156; Gaps 17;

QY 1 MFGKRKRVEISAPSNFHRVHTGPDQHEQKFTGLPRQWOSLIESARRPKPLVDPAKIT 60
Db 1 MFGKKKKKIEISGPNFHRVHTGPDQHEQKFTGLPRQWOSLIESARRPKPLVDPAKIT 60

QY 61 STQPGAPKTVIRGSKGAKDGAULTLLDDEFENSVTSNLSLRDPSPPPARA-----R 112
Db 61 PQLAPMKTVIRGNKPKETSINGLLEDFENSVTSNLSLRKESPPTPDQAGSSHGFGHA 120

QY 113 QENGM-----PEEPATTA-----RGG-----PGKA 132
Db 121 EENGFTTFQSYSSSDTTADYITEKYREKSLYGDGDDLDPPYRGSHAAKQNGHVMKMGHEA 180

QY 133 -----GSGRPFAGH-----SEAG 145
Db 181 YYSEVFKPLKSDFAFSAHYHSLDLSKPSSEYDLKWEYGRASSSPFLDYSFQFTPSRTA 240

QY 146 GSGGDRRA-----GP-----EKRPKSRREGSGGQESSRDKPLSGPDVGTQPPAG 192
Db 241 GTSGCKESLAYSESEWSPGLDDYDRRRPKSYLYNOTSPQTMK-QRSRSGSLQEPMMSF 299

QY 193 LASGAKL-AAGRPNTY-----PRADTDH-----PSRGAQGEHPHVPNGP 232
Db 300 GASAFKTHPQGHYSNYSYTPRLSEPTMCIPKVDYDRAQMVLSPLSGS-----DTPRGP 354

QY 233 SAGGLAIPOS-----SSSSSRPPTRAGAPSPGVLGPHASEPQLAPPACTP----- 278
Db 355 A-----KLQSQKSGYSSSSSHQVPSGYHKA-----TLYHPSLQSSSQYSTASLSSLSL 406

QY 279 AAPAVPGPGRSPQEPQVSHQFRAALQLVVDGPDPRSILDNFKIGSGTIVCIAT 338
Db 407 SSSSTPPPSGWSSSDQDQPSRVSHQFRAALQLVVDGPDPRSILDNFKIGSGTIVCIAT 466

QY 339 TVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFL 398

Db 467 TEKHTGKQVAVKMDLRKQORRELLFNEVWIMRDYHHDNVDMVNSYLVGDELWVMEFL 526
Qy 399 EGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHHRDKSDSILLTHDGRVKLSD 458
Db 527 EGGALTDIVTHTRMNEEQIATVCLSVLRALSVLHNGQVHHRDKSDSILLTSDGRVKLSD 586
Qy 459 FGFCQVSKVEPRKSLVGTPTWMAPELISRLPYGPEVDIWSLGIWVEMVDGEPPEYFNE 518
Db 587 FGFCQVSKVEPRKSLVGTPTWMAPEVLSRLPYGTEVDIWSLGIWVEMIDGEPPEYFNE 646
Qy 519 PPLKAMKMRDMLPRLKLNHLKVSPLSGFLDRLVLRDPAQATAAELLLKHPFLKAGPP 578
Db 647 PPLQAMRRIRDSLPVRVKDLHKVSSVLGRFLDMLVREPSQRATAGELLGHPFLKAGPP 706
Qy 579 ASIVPLMRQNR 589
Db 707 SCIVPLMRQYR 717
RESULT 10
ID AAB65705 standard; protein; 719 AA.
AC AAB65705;
DT 27-MAR-2001 (first entry)
DE Novel protein kinase, SEQ ID NO: 234.
KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
KW dermatological; antidiabetic; antinfertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
OS Homo sapiens.
XX WO200073469-A2.
XX 07-DEC-2000.
XX 26-MAY-2000; 2000WO-US014842.
XX 28-MAY-1999; 99US-0136503P.
XX (SUGEN-) SUGEN INC.
XX Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX WPI; 2001-032161/04.
XX N-PSDB; AAF44734.
XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers.
PS Claim 10; Fig 1; 310pp; English.
XX The present sequence is a novel protein kinase. The novel protein kinases
CC and the nucleic acids that encode them may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-

CC stress related disorders, chronic inflammatory bowel disease, chronic
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
CC disorders
XX Sequence 719 AA;
SQ Query Match 56.0%; Score 1731; DB 4; Length 719;
Best Local Similarity 52.4%; Pred. No. 2.6e-117;
Matches 383; Conservative 66; Mismatches 126; Indels 156; Gaps 17;
Qy 1 MFGKKKRVESAPNFEHVRHTGPDQHEQKFTGLPRQWOSLIESARRPKPLVDPACT 60
Db 1 MFGKKKKIEISGPNFHRVHTGPDQEQKFTGLPQQWHSLLADTANRKPMPVDFSCIT 60
Qy 61 STQCGAPKTVIRGSGKAGDGLTLLDFENMSVTRSNLSLRDSDPPPPARA-----R 112
Db 61 PIQLAPMKTIIVRGNPKCKETSINGLLEDFNISVTRSNLSRKESPTPDQGASSHGPHGA 120
Qy 113 QENGM-----PEEPATTA-----RGG-----PGKA 132
Db 121 BENGFIITFSQYSSSESDTTADYTKVREKSLYGGDLLDPYRGSHAAKQNGHVMMKMGHA 180
Qy 133 -----GSRGRFAGH-----SEAG 145
Db 181 YYSEVKPLKSDPARFSADYHSHLDSLSKPSSEYSDLKWEYQRASSSSPLDYSFQTPSRTA 240
Qy 146 GSGSDRRRA-----GP-----EKRPKSSREGSGGPOESSRDKRPLSGPDVGTP-QPA 191
Db 241 GTSGCKSLAYSESEWGPSSLDYDRRPKSSVLYNOTSPQPTWR-QRSRSGSLQBPMPWF 299
Qy 192 GLASGAKLAAGAPFNNTY-----PRADTDH-----PSRGAQGEHVDVAPNGP 232
Db 300 GASAKFTHPQGHSYNSYTYPRLSEPTMCPKVYDRAQWVLSPPLSGS-----DTYPRGP 354
Qy 233 SAGGLAIPOS-----SSSSSRPPTRAKGAPSGVLGPHASEPQIAPPACTP----- 278
Db 355 A-----KLPSQSKSGYSSSSHQYPSGYHKA-----TLYHPSLQSSSQYISTASYLSLSL 406
Qy 279 AAPAVGPPGPRSPQEPORVSHEQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCTA 338
Db 407 SSSYTPPSPWSSSSDQPSRVSHEQFRAALQLVSPGDPREYLANFIKIGEGSTGIVCTA 466
Qy 339 TVRSSGKLVAVKMDLRKQORRELLFNEVWIMRDYOHENNVEMVNSYLVGDELWVMEFL 398
Db 467 TEKHTGKQVAVKMDLRKQORRELLFNEVWIMRDYHHDNVDMVNSYLVGDELWVMEFL 526
Qy 399 EGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHHRDKSDSILLTHDGRVKLSD 458
Db 527 EGGALTDIVTHTRMNEEQIATVCLSVLRALSVLHNGQVHHRDKSDSILLTSDGRVKLSD 586
Qy 459 FGFCQVSKVEPRKSLVGTPTWMAPELISRLPYGPEVDIWSLGIWVEMVDGEPPEYFNE 518
Db 587 FGFCQVSKVEPRKSLVGTPTWMAPEVLSRLPYGTEVDIWSLGIWVEMIDGEPPEYFNE 646
Qy 519 PPLKAMKMRDMLPRLKLNHLKVSPLSGFLDRLVLRDPAQATAAELLLKHPFLKAGPP 578
Db 647 PPLQAMRRIRDSLPVRVKDLHKVSSVLGRFLDMLVREPSQRATAGELLGHPFLKAGPP 706
Qy 579 ASIVPLMRQNR 589
Db 707 SCIVPLMRQYR 717
RESULT 11
ADC37451
ID ADC37451 standard; protein; 719 AA.
XX ADC37451;
XX 18-DEC-2003 (first entry)
XX Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 284.
DE

XX Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
 KW cancer; infectious disease; bone disease; AIDS; Antiinflammatory;
 KW neurodegenerative disease; ischaemic disorder; Antimicrobial; Osteopathic; Anti-HIV;
 KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
 KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human.
 XX Homo sapiens.
 XX WO2003048202-A2.
 XX 12-JUN-2003.
 XX 03-DEC-2002; 2002WO-JP012644.
 XX 03-DEC-2001; 2001JP-00368692.
 XX 05-DEC-2001; 2001US-03358299.
 XX 03-OCT-2002; 2002JP-00291302.
 XX 04-OCT-2002; 2002US-0415769P.
 XX (ASAH) ASAH KASEI KK.
 XX Matsuda A, Muramatsu S;
 XX WPI; 2003-505282/47.
 XX N-PSDB; ADC37450.
 XX New purified protein that activates nuclear factor kappa B (NF-kappaB),
 PT useful for treating inflammation, autoimmune diseases, cancers,
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
 PT ischemic disorders.
 XX Claim 1; SEQ ID NO 284; 938pp; English.
 XX The present invention relates to novel proteins and their coding
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
 CC kappaB). The proteins and their coding sequences are useful for treating
 CC a disease associated with NF-kappaB activation, such as inflammation,
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
 CC neurodegenerative diseases, or ischaemic disorders.
 XX Sequence 719 AA;
 SQ

Query Match 56.0%; Score 1731; DB 7; Length 719;
 Best Local Similarity 52.4%; Pred. No. 2.6e-117;
 Matches 383; Conservative 66; Mismatches 126; Indels 156; Gaps 17;

QY 1 MFGKKRKRVEISAPNFEHRVHTGPDQHEQKFTGLPRQMSLIEESARRPKPLVDPCIT 60
 DB 1 MFGKKKKKIEISGPNFEHRVHTGPDQHEQKFTGLPRQMSLIEESARRPKPLVDPCIT 60
 QY 61 STQPGAPKTIIVRGSKGAKGALTLTLDPEPNMVSRTSNLSLRDPPPPARA-----R 112
 DB 61 PIQLAPMKTIIVRGSKPKCKETSINGLLEDFDNTSVTRSNLSLRKESPTPDQGASHGHGA 120
 QY 113 QENGM-----PEEPATTA-----RGG-----PGKA 132
 DB 121 EENGFTTFQYSESSTTDADYTEKREKSLYGLDDLDPIYRGSHAQKQNHVWKMKGHA 180
 QY 133 -----GSRGRFAGH-----SEAG 145
 DB 181 YYSEVKPLKSDFAFSAADYHSLDLSKPSSEYSDLKWEYGRASSSSPLDYSFQFTSRTA 240
 QY 146 GSGCDRRRA-----GP-----EKRPKSSRGSGGPGQESSRDKRPLSGPDVGTGTP-QPA 191
 DB 241 GTSGCSKESLAYSESEWGPGLDDYDRPKKSSYLNTSQPTMR-QRSRSGSGIQLPEPMMPF 299
 QY 192 GLASGAKLAAGRPFNTY-----PRADTDH-----PSRGAQEPHDVAPNGP 232
 DB 300 GASAFKTHPGQHSYNSYTYPRLSPEPTMCPKVYDRAQMWLSPPLSGS-----DTYPRGP 354
 QY 233 SAGGLAIPQS-----SSSSSRPPTTRAGAPSPGVLGPHASEPQLAPPACTP----- 278

Db 355 A-----KLPOQSKSGYSSSSHQYPSGYHKA-----TLYHHPSLQSSQYISTASYLSLSL 406
 QY 279 AAPAVPGPPGPRSPQREPORVSHEQFRAALQIIVDPGPRSYLDNFIKIGEGSTGIVCIA 338
 Db 407 SSSTYPFPPSWGSSSQPSRVSHQFRAALQIIVDPGPRSYLDNFIKIGEGSTGIVCIA 466
 QY 339 TVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYOHENNVEMVNSYLVGDELWVWMEFL 398
 Db 467 TEKHTGKQVAVKMDLRKQORRELLFNEVIMRDYOHENNVEMVNSYLVGDELWVWMEFL 526
 QY 399 EGGALTDIVTHTRMNEEQIAAVALQALSVLHQAQGVHHRDIKSDSILLTTHDGRVKLS 458
 Db 527 EGGALTDIVTHTRMNEEQIATVCLSVLRALSVLHQAQGVHHRDIKSDSILLTSDGRVKLS 586
 QY 459 FGFCQVSKVEPKRSLVGTTPYMAPELISRLPYGPEVDIWSLGIWVEMVNGEPPYFNE 518
 Db 587 FGFCQVSKVEPKRSLVGTTPYMAPEVISRLPYGTEVDIWSLGIWVEMVNGEPPYFNE 646
 QY 519 PPLKAMKMRDNLPPRLKNLHKVPSLKGFLDRLVDRDPAQRATAAELLKHPFLAKAGPP 578
 Db 647 PPLQAMRRIRDSLPVRKDLHKVSSVLRGFLDMLVREPSQRATAGELLGHFPLKLAGPP 706
 QY 579 ASIVFLMRQNR 589
 Db 707 SCIVPLMRQYR 717
 XX AAE02187;
 DT 10-AUG-2001 (first entry)
 XX Human p21-activated kinase 5 (PAK5) protein.
 DE Human; p21-activated kinase 5; PAK5; genetic mapping; neuroprotective;
 KW immunosuppressive; gene therapy; cancer; angiogenesis-related disorder;
 KW serine-threonine kinase; restriction fragment length polymorphism; RFLP;
 KW central nervous system disorder; immune-related disorder; cytostatic.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Domain II..53
 FT /label= GBD/CRIB_motif
 FT Domain 449..700
 FT /label= Kinase_catalytic_domain
 FT Domain 456..463
 FT /label= Kinase_subdomain_I
 FT Domain 476..478
 FT /label= Kinase_subdomain_II
 FT Domain 611..613
 FT /label= Kinase_subdomain_VIII
 FT Domain 625..630
 FT /label= Kinase_subdomain_IX
 XX WO200136602-A2.
 PN 25-MAY-2001.
 XX 14-NOV-2000; 2000WO-EP010736.
 XX 15-NOV-1999; 99US-00439756.
 XX (PHAA) PHARMACIA & UPJOHN SPA.
 XX Dahlberg M, Moll J, Galvani A;
 XX WPI; 2001-355626/37.
 XX N-PSDB; AAD06418.

QY 480 YWMAPELISRLPGPVDIWSLGIWVIMVGDGPPYFNEPPLKAMKMDIPLPRLKLNH 539
 Db 182 YWMAPELISRLPGPVDIWSLGIWVIMVGDGPPYFNEPPLKAMKMDIPLPRLKLNH 241
 QY 540 KVSPLKGLFDRLLVRDPAQRATAAEALLKHPFLAKAGPPASIVPLMRQNR 591
 Db 242 KVSPLKGLFDRLLVRDPAQRATAAEALLKHPFLAKAGPPASIVPLMRQNR 293

RESULT 14
 AAY55940
 ID AAY55940 standard; protein; 681 AA.
 XX
 AC AAY55940;
 XX
 DT 18-FEB-2000 (first entry)
 XX
 DE Human PAK4 protein.
 KW Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic;
 KW antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;
 KW neuroprotective; cardiac; cerebroprotective; cytotstatic; antidiabetic;
 KW vulnery; STE20; protein kinase; STLK3; STLK4; STLK5; STLK6; STLK7;
 ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GSK2; PAK4; PAK5; antagonist;
 KW antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
 KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
 KW rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
 KW myocardial infarction; cardiovascular disease; stroke; renal failure;
 KW oxidative stress-related neurodegenerative disorder; Parkinson's disease;
 KW amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
 KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
 KW mesangial disorder; growth regulation; wound healing; T cell activation;
 KW immunosuppressant.
 XX
 OS Homo sapiens.
 XX
 PN WO9553036-A2.
 XX
 PD 21-OCT-1999.
 XX
 PF 13-APR-1999; 99WO-US008150.
 XX
 PR 14-APR-1998; 98US-0081784P.
 XX
 PA (SUG-) SUGEN INC.
 XX
 PI Plowman G, Martinez R, Whyte D;
 XX
 DR WPI; 1999-611301/52.
 DR N-PSDB; AA240492.
 XX
 PT Novel kinase-related polypeptides used for the diagnosis and treatment of
 XX kinase-related diseases and disorders.
 PS
 PS Claim 11; Page 308-310; 387pp; English.
 XX
 CC This sequence represents a novel STE20-related protein kinase. The
 CC invention relates to nucleic acid molecule encoding a kinase polypeptide
 CC selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3,
 CC ZC4, KHS2, SULU1, SULU3, GSK2, PAK4 and PAK5. The proteins are used to
 CC identify agonists and antagonists, and to raise antibodies. The
 CC polynucleotides are useful in gene therapy protocols. The polynucleotides,
 CC polypeptides, antibodies, antagonists and agonists may be used to treat
 CC diseases such as immune-related disorders and diseases (e.g. rheumatoid
 CC arthritis, artherosclerosis, chronic inflammatory bowel disease (e.g.
 CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
 CC rhinitis, autoimmunity, and organ transplantation, chronic inflammatory
 CC pelvic disease, multiple sclerosis, organ transplantation, myocardial
 CC infarction, cardiovascular disease, stroke, renal failure, oxidative
 CC stress-related neurodegenerative disorders (e.g. amyotrophic lateral
 CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,
 CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
 CC mellitus, fibrotic and mesangial disorders. The proteins may also be

CC useful for cell growth regulation (e.g. in wound healing), T cell
 CC activation, mitosis control, and as immunosuppressants
 XX
 SQ Sequence 681 AA;
 Query Match 47.7%; Score 1473.5; DB 2; Length 681;
 Best Local Similarity 48.1%; Pred. No. 1.3e-98;
 Matches 331; Conservative 69; Mismatches 169; Indels 119; Gaps 12;
 QY 4 KKKKRVETISAPSNFHRVHTGFDQHQKFTGLPRQWQSLIESARRPKLVDPACITSIQ 63
 Db 5 KKKGRPEISAPQNFQHRVHTSFDPKGKGVGLPQMQNIL-DTLRRPKVWDPSTRIVQ 63
 QY 64 PGAPKTVIRGSGAKDGLTLLLDPEPNMVSRTNSLRDSDPPPPAR- 112
 Db 64 LQPMKTVVRGSAAMPVDGYISGLLNDIQKLSVSSNTLGRSPTSRRAQSLGLLGDHWA 123
 QY 113 -----QENQM-----PEEPATTARGGPGKAGSRG-- 136
 Db 124 TDPDMYLQSPQSERTDPHGLYLSGNGTTPAGHKQMPWPEPQSPRVLPNGLAAKAAQSLGPA 183
 QY 137 RPAHSEAG---GGSDRRRAGPEKPKSRRSGSGQPSRRDKRPLS-----GP 183
 Db 184 EFQASQRCQLGACLQSPGASPTGTNRHGMKAAKHGSEEARPQSCLVGSATGRPGG 243
 QY 184 DVGTPOPAGLAGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVAENGPSAGGLAIPQSS 243
 Db 244 E-GSPSPKTRRESLKRLLFRSM-FLSTAATAPSSSKPGPPQSKN----- 288
 QY 244 SSSSRPP-----TRAGAPSP---GVLGPHASEPOLAPPACTPAAPVPGPPGPRS 291
 Db 289 -SFRPPEKNDPPSLVAKAQSPLSDQPVGTFTPLTTSSTSSPKSLRTAPATQQLPGRSS 347
 QY 292 PQEPOR-----VSHEQFRAALQLVDPGDRSYL 321
 Db 348 PAPSPTWHAQISTSNLYLPQDPTVAKGALAGEDTGVVTHEQKALRMVWDQDPRLL 407
 QY 322 DNFIKIGEGSTGIVCIATVRSRSGKLVAKMDLRKQORRELLFNEVVIWDYQHNWVEM 381
 Db 408 DSVKLGEGSTGIVCLAREKHSRQVAVKMDLRKQORRELLFNEVVIWDYQHNWVEM 467
 QY 382 YNSLYGDELWVVMFELEGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHAGVTHRDI 441
 Db 468 YKSYLVGEELWLMFELQGGALTDIVSVQVRLNEEQIATVCEAVLQALAVLHAGVTHRDI 527
 QY 442 KSDSILLTHDGRVKLSDFGFCQAVSKEVPRRSKLVCTPYWMAPELISRLPYGGEVWISL 501
 Db 528 KSDSILLTHDGRVKLSDFGFCQAVSKEVPRRSKLVCTPYWMAPEVISRSLYATEVWISL 587
 QY 502 GIMVIMVGDGPPYFNEPPLKAMKMDIPLPRLKLNHVKVPSLKGFLDLRLVRDPAQRA 561
 Db 588 GIMVIMVGDGPPYFSDSPVQAMKRLRDSPPPKLNKSHKVSPIRDLFLERMLVRDQERA 647
 QY 562 TAAELKHPFLAKAGPPASIVPLMRQNR 589
 Db 648 TAQELDHPFLLQTGLPECLVPLIQLYR 675

RESULT 15
 AAB03967
 ID AAB03967 standard; protein; 681 AA.
 XX
 AC AAB03967;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE Signal transduction serine/threonine protein kinase.
 KW Signal transduction serine threonine protein kinase; kinase; modulation;
 KW signal transduction; antisense; diagnosis; detection; treatment;
 KW antibody; inflammatory disease; macrophage regulation;
 KW endothelial cell regulation; angiogenesis; peripheral vascular disease;
 KW secretion; apoptosis; atherosclerosis; neurodegenerative processes;

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OM protein - protein search, using sw model

Run on: September 29, 2004, 17:58:42 ; Search time 40.8485 Seconds
(without alignments)
746.929 Million cell updates/sec

Title: US-10-693-367-2

Perfect score: 3090

Sequence: 1 MFGKKRKRVEISAPNSFHR.....LAKAGPPASIVPLMRQNR 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTUS COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3090	100.0	591	3	US-09-082-737-2
2	3090	100.0	591	4	US-09-688-188B-103
3	3090	100.0	591	4	US-09-718-032-2
4	3090	100.0	591	4	US-09-291-417D-103
5	2073	67.1	398	4	US-09-688-188B-30
6	2073	67.1	398	4	US-09-291-417D-30
7	1473.5	47.7	681	4	US-09-688-188B-29
8	1473.5	47.7	681	4	US-09-291-417D-29
9	1470.5	47.6	681	4	US-09-765-815-2
10	1277	41.3	250	3	US-09-082-737-3
11	1277	41.3	250	4	US-09-718-032-3
12	912	29.5	544	2	US-08-935-760-2
13	907	29.4	544	4	US-09-688-188B-95
14	907	29.4	544	4	US-09-291-417D-95
15	900	29.1	524	2	US-08-615-942A-2
16	900	29.1	524	4	US-09-237-325-2
17	899	29.1	544	3	US-08-559-397A-19
18	894	28.9	506	1	US-08-369-780-2
19	894	28.9	506	1	US-08-475-682-2
20	894	28.9	506	1	US-08-780-833-2
21	894	28.9	506	1	US-08-636-036-2
22	894	28.9	506	3	US-08-918-509-2
23	894	28.9	506	3	US-09-108-262-2
24	894	28.9	506	4	US-09-688-188B-94
25	894	28.9	506	4	US-09-291-417D-94
26	891.5	28.9	545	2	US-08-935-760-4
27	891.5	28.9	545	4	US-09-688-188B-93

28	891.5	28.9	545	4	US-09-291-417D-93	Sequence 93, Appl
29	867	28.1	544	3	US-08-559-397A-29	Sequence 29, Appl
30	849	27.5	544	3	US-08-559-397A-30	Sequence 30, Appl
31	833.5	27.0	465	2	US-08-114-555A-2	Sequence 2, Appl
32	821	26.6	694	3	US-08-559-397A-31	Sequence 31, Appl
33	814.5	26.4	465	3	US-08-559-397A-2	Sequence 2, Appl
34	804	26.0	305	4	US-09-765-815-10	Sequence 10, Appl
35	782	25.3	793	3	US-09-588-256-10	Sequence 10, Appl
36	769	24.9	268	2	US-08-852-743-3	Sequence 3, Appl
37	769	24.9	268	3	US-09-185-370-3	Sequence 3, Appl
38	741	24.0	250	4	US-09-718-032-4	Sequence 4, Appl
39	719.5	23.3	244	4	US-09-163-507-1	Sequence 1, Appl
40	717.5	23.2	271	2	US-08-852-743-4	Sequence 4, Appl
41	717.5	23.2	271	3	US-09-185-370-4	Sequence 4, Appl
42	712	23.0	245	4	US-09-163-507-3	Sequence 3, Appl
43	706	22.8	244	4	US-09-163-507-2	Sequence 2, Appl
44	704	22.8	251	3	US-09-082-737-5	Sequence 5, Appl
45	699	22.6	250	4	US-09-718-032-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-082-737-2
; Sequence 2, Application US/09082737
; Patent No. 6013500
; GENERAL INFORMATION:
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4; A No. 6013500el Gene Encoding A Serine/
; TITLE OF INVENTION: Threonine Kinase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11230
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,737
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/55311
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-082-737-2

Query Match 100.0%; Score 3090; DB 3; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.3e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGKKRKRVEISAPNSFHRVHTGPDHQKFTGLPRQWQSLIESARRPKPLVDPACIT 60
Db 1 MFGKKRKRVEISAPNSFHRVHTGPDHQKFTGLPRQWQSLIESARRPKPLVDPACIT 60
QY 61 STQPGAPKTVRGSGAKDGKALTLLDFFENNVSTRSLRDSPPPARAPQENGMBEE 120

Db 61 SIQCAPKTIVRGSKGAKDGALITLLDEFENMSVTRSNLSRRDSDPPPARAQENGMPPEE 120
QY 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRRAGPEKRPKSSREGSGGPOESSDRKRLP 180
Db 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRRAGPEKRPKSSREGSGGPOESSDRKRLP 180
QY 181 SGPDVGTTPQAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGEHVDVAPNGPSAGGLAIP 240
Db 181 SGPDVGTTPQAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGEHVDVAPNGPSAGGLAIP 240
QY 241 QSSSSSSRPPTTRARGAPSGVLGHASEPQLAPPACTPAAPVAPGPPGPRSPQREPORVS 300
Db 241 QSSSSSSRPPTTRARGAPSGVLGHASEPQLAPPACTPAAPVAPGPPGPRSPQREPORVS 300
QY 301 HQFRAALQLVVDPGDPRSILDNFKIGEGSTGIICATVRSGLKLVAKKMDLRKQRR 360
Db 301 HQFRAALQLVVDPGDPRSILDNFKIGEGSTGIICATVRSGLKLVAKKMDLRKQRR 360
QY 361 ELLFNEVIMRDYQHENVVEMVNSYLVDGLMVMVEFLEGGALTDIVTHTRMNEEQIAAV 420
Db 361 ELLFNEVIMRDYQHENVVEMVNSYLVDGLMVMVEFLEGGALTDIVTHTRMNEEQIAAV 420
QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPT 480
Db 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPT 480
QY 481 WNAPELISRLPYGPEVDIWSLGIWVEMVVDGPPYFNEPPLKAMKMIRODNLPPRLKNLHK 540
Db 481 WNAPELISRLPYGPEVDIWSLGIWVEMVVDGPPYFNEPPLKAMKMIRODNLPPRLKNLHK 540
QY 541 VSPSLKGFLLDRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
Db 541 VSPSLKGFLLDRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

RESULT 2

US-09-688-188B-103
; Sequence 103, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT FILING DATE: 2000-10-16
; PRIOR FILING DATE: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 103
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-103

Query Match 100.0%; Score 3090; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.3e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGRKKRVEISAPSNFHRVHTGFDQHEOKFTGLPRQWOSLIEESARRPKPLVDPAKIT 60
Db 1 MFGRKKRVEISAPSNFHRVHTGFDQHEOKFTGLPRQWOSLIEESARRPKPLVDPAKIT 60
QY 61 SIQCAPKTIVRGSKGAKDGALITLLDEFENMSVTRSNLSRRDSDPPPARAQENGMPPEE 120
Db 61 SIQCAPKTIVRGSKGAKDGALITLLDEFENMSVTRSNLSRRDSDPPPARAQENGMPPEE 120
QY 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRRAGPEKRPKSSREGSGGPOESSDRKRLP 180
Db 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRRAGPEKRPKSSREGSGGPOESSDRKRLP 180

Db 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRRAGPEKRPKSSREGSGGPOESSDRKRLP 180
QY 181 SGPDVGTTPQAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGEHVDVAPNGPSAGGLAIP 240
Db 181 SGPDVGTTPQAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGEHVDVAPNGPSAGGLAIP 240
QY 241 QSSSSSSRPPTTRARGAPSGVLGHASEPQLAPPACTPAAPVAPGPPGPRSPQREPORVS 300
Db 241 QSSSSSSRPPTTRARGAPSGVLGHASEPQLAPPACTPAAPVAPGPPGPRSPQREPORVS 300
QY 301 HQFRAALQLVVDPGDPRSILDNFKIGEGSTGIICATVRSGLKLVAKKMDLRKQRR 360
Db 301 HQFRAALQLVVDPGDPRSILDNFKIGEGSTGIICATVRSGLKLVAKKMDLRKQRR 360
QY 361 ELLFNEVIMRDYQHENVVEMVNSYLVDGLMVMVEFLEGGALTDIVTHTRMNEEQIAAV 420
Db 361 ELLFNEVIMRDYQHENVVEMVNSYLVDGLMVMVEFLEGGALTDIVTHTRMNEEQIAAV 420
QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPT 480
Db 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPT 480
QY 481 WNAPELISRLPYGPEVDIWSLGIWVEMVVDGPPYFNEPPLKAMKMIRODNLPPRLKNLHK 540
Db 481 WNAPELISRLPYGPEVDIWSLGIWVEMVVDGPPYFNEPPLKAMKMIRODNLPPRLKNLHK 540
QY 541 VSPSLKGFLLDRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
Db 541 VSPSLKGFLLDRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

RESULT 3

US-09-718-032-2
; Sequence 2, Application US/09718032
; Patent No. 6657168
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
; FILE REFERENCE: 575/55311-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/718,032
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11341
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/082,737
; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 2
; LENGTH: 591
; TYPE: PRT
; ORGANISM: human
US-09-718-032-2

Query Match 100.0%; Score 3090; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.3e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGRKKRVEISAPSNFHRVHTGFDQHEOKFTGLPRQWOSLIEESARRPKPLVDPAKIT 60
Db 1 MFGRKKRVEISAPSNFHRVHTGFDQHEOKFTGLPRQWOSLIEESARRPKPLVDPAKIT 60
QY 61 SIQCAPKTIVRGSKGAKDGALITLLDEFENMSVTRSNLSRRDSDPPPARAQENGMPPEE 120
Db 61 SIQCAPKTIVRGSKGAKDGALITLLDEFENMSVTRSNLSRRDSDPPPARAQENGMPPEE 120
QY 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRRAGPEKRPKSSREGSGGPOESSDRKRLP 180
Db 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRRAGPEKRPKSSREGSGGPOESSDRKRLP 180
QY 181 SGPDVGTTPQAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGEHVDVAPNGPSAGGLAIP 240
Db 181 SGPDVGTTPQAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGEHVDVAPNGPSAGGLAIP 240

QY 241 QSSSSSRPPTTRAGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPRSPQREPORVS 300
DB 241 QSSSSSRPPTTRAGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPRSPQREPORVS 300
QY 301 HEQFRAALQLVDPGPRSYLNDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQRR 360
DB 301 HEQFRAALQLVDPGPRSYLNDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQRR 360
QY 361 ELLFNEVIMRDYQHENVVMYNSYLVGDELWVMEFLEGALTDIVTHRMNEEQIAAV 420
DB 361 ELLFNEVIMRDYQHENVVMYNSYLVGDELWVMEFLEGALTDIVTHRMNEEQIAAV 420
QY 421 CLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPVRKSLVGTPT 480
DB 421 CLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPVRKSLVGTPT 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWVEMVDPGPPYFNEPPLKAMKMIKMDLPPRLKNLHK 540
DB 481 WMAPELISRLPYGPEVDIWSLGIWVEMVDPGPPYFNEPPLKAMKMIKMDLPPRLKNLHK 540
QY 541 VSPSLKGFLLRDLVRDPAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
DB 541 VSPSLKGFLLRDLVRDPAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

RESULT 4

US-09-291-417D-103
; Sequence 103, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 103
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-103

Query Match 100.0%; Score 3090; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.3e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGKRRKVEISAPSNFHRVHTGFDQHQKFTGLPRQWOLIESARRPKPLVDPACT 60
DB 1 MFGKRRKVEISAPSNFHRVHTGFDQHQKFTGLPRQWOLIESARRPKPLVDPACT 60
QY 61 STQPGAPKTIIVRGSKAKDGALTLLEDENFMSVTRNSLRDPSPPPARAGQNGMPEE 120
DB 61 STQPGAPKTIIVRGSKAKDGALTLLEDENFMSVTRNSLRDPSPPPARAGQNGMPEE 120
QY 121 PATTARGGPKAGSRGRFAGHSEAGGSDRRRAGPEKPKSRREGSGGQPSRRDKRPL 180
DB 121 PATTARGGPKAGSRGRFAGHSEAGGSDRRRAGPEKPKSRREGSGGQPSRRDKRPL 180
QY 181 SGPDVCTPQAGLASAKLAAGRPFTYPRADTDHPSRGAQGEPHDVAENGPSAGGLAIP 240
DB 181 SGPDVCTPQAGLASAKLAAGRPFTYPRADTDHPSRGAQGEPHDVAENGPSAGGLAIP 240
QY 241 QSSSSSRPPTTRAGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPRSPQREPORVS 300
DB 241 QSSSSSRPPTTRAGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPRSPQREPORVS 300
QY 301 HEQFRAALQLVDPGPRSYLNDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQRR 360

DB 301 HEQFRAALQLVDPGPRSYLNDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQRR 360
QY 361 ELLFNEVIMRDYQHENVVMYNSYLVGDELWVMEFLEGALTDIVTHRMNEEQIAAV 420
DB 361 ELLFNEVIMRDYQHENVVMYNSYLVGDELWVMEFLEGALTDIVTHRMNEEQIAAV 420
QY 421 CLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPVRKSLVGTPT 480
DB 421 CLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPVRKSLVGTPT 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWVEMVDPGPPYFNEPPLKAMKMIKMDLPPRLKNLHK 540
DB 481 WMAPELISRLPYGPEVDIWSLGIWVEMVDPGPPYFNEPPLKAMKMIKMDLPPRLKNLHK 540
QY 541 VSPSLKGFLLRDLVRDPAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
DB 541 VSPSLKGFLLRDLVRDPAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

RESULT 5

US-09-688-188B-30
; Sequence 30, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 30
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-30

Query Match 67.1%; Score 2073; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.3e-126;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 ASGAKLAAGRPFTYPRADTDHPSRGAQGEPHDVAENGPSAGGLAIPQSSSSSRPPTRA 253
DB 1 ASGAKLAAGRPFTYPRADTDHPSRGAQGEPHDVAENGPSAGGLAIPQSSSSSRPPTRA 253
QY 254 RGAPSPVLGPHASEPQLAPPACTPAAPAVPGPPGPRSPQREPORVSHEQFRAALQLVVD 313
DB 61 RGAPSPVLGPHASEPQLAPPACTPAAPAVPGPPGPRSPQREPORVSHEQFRAALQLVVD 120
QY 314 PGDPRSVDLNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQRRLLFNEVIMRDY 373
DB 121 PGDPRSVDLNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQRRLLFNEVIMRDY 180
QY 374 QHENVVMYNSYLVGDELWVMEFLEGALTDIVTHRMNEEQIAAVCLAVLQALSVLHA 433
DB 181 QHENVVMYNSYLVGDELWVMEFLEGALTDIVTHRMNEEQIAAVCLAVLQALSVLHA 240
QY 434 QGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPVRKSLVGTPTWMAPELISRLPYG 493
DB 241 QGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPVRKSLVGTPTWMAPELISRLPYG 300
QY 494 PEVDIWSLGIWVEMVDPGPPYFNEPPLKAMKMIKMDLPPRLKNLHKVPSLKGFLDRLL 553
DB 301 PEVDIWSLGIWVEMVDPGPPYFNEPPLKAMKMIKMDLPPRLKNLHKVPSLKGFLDRLL 360
QY 554 VRDPAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

Db 361 VRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNR 398
|||||

RESULT 6

US-09-291-417D-30
; Sequence 30, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 1999-04-13
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-30

Query Match 67.1%; Score 2073; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.3e-126; Indels 0; Gaps 0;
Matches 398; Conservative 0; Mismatches 0;

QY 194 ASGAKLAAGRPNTYPRADTDHPSRGAQGEHDVAPNGPSAGGLAIPQSSSSSRPPTRA 253
Db 1 ASGAKLAAGRPNTYPRADTDHPSRGAQGEHDVAPNGPSAGGLAIPQSSSSSRPPTRA 60
QY 254 RGAPSGVLGPHASEPOLAPPACTPAAPVPGPGPSQRPQVSHQFPAALQLVVD 313
Db 61 RGAPSGVLGPHASEPOLAPPACTPAAPVPGPGPSQRPQVSHQFPAALQLVVD 120
QY 314 PGDPRSYLNFNFKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVIMRDY 373
Db 121 PGDPRSYLNFNFKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVIMRDY 180
QY 374 QHENVVMYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEBQIAAVCLAVLQALSVLHA 433
Db 181 QHENVVMYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEBQIAAVCLAVLQALSVLHA 240
QY 434 QGVHRIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSILVGTPTYWMAPELISRLPYG 493
Db 241 QGVHRIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSILVGTPTYWMAPELISRLPYG 300
QY 494 PEVDIWSLGIWVIMVEMVDGPPYFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFIDRL 553
Db 301 PEVDIWSLGIWVIMVEMVDGPPYFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFIDRL 360
QY 554 VRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNR 591
Db 361 VRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNR 398

RESULT 7

US-09-688-188B-29
; Sequence 29, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14

; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-29

Query Match 47.7%; Score 1473.5; DB 4; Length 681;
Best Local Similarity 48.1%; Pred. No. 3.1e-87;
Matches 331; Conservative 69; Mismatches 169; Indels 119; Gaps 12;

QY 4 KKKRVEISAPSNFHRVHTGFDQHEOKFTGLPROMQSLIEESARRPKPLVDPAITSIQ 63
Db 5 KKKRPEISAFONFQHRVHTSFDKGEKFGVGLPPQWQNIL-DTLRRPEVVDPSIRIVQ 63
QY 64 PGAPKTIIVRGSKGAKDGALTLLDEFENNSVTRNSLRDSDPPPARAR----- 112
Db 64 LQPMKTVVRGSAAMPVDGYISGLNDIQKLSVISSNTLRGSRPTSRRAQSLGLLGDHWA 123
QY 113 -----QENG-----PEPATARGCPKAGSRG-- 136
Db 124 TDDMYLQSPQSERTDPHGLYLSCNGGTPAGHKQMPPEQSPRVLPNGLAAKAQSLGA 183
QY 137 RFAGHSEAG---GGSGDRRRAGPERKPKSSREGSGGPOESSRDKRPLS-----GP 183
Db 184 EFGQASQRLQLGACLQSPFGASPTGTNRHGKAAKHGSEARPOSCLVGSATCRPG 243
QY 184 DVGTPQPAAGLASKAKLAAGRPNVTPRADTDHPSRGAQGEHDVAPNGPSAGGLAIPQS 243
Db 244 E-GSPSPKTRSSSLKRRLFRSM-FLSTAATAPPSSSKPGPPQSKPN----- 288
QY 244 SSSSP-----TPARGAPSP---GVLGPHASEPOLAPPACTPAAPVPGPPGPS 291
Db 289 -SSFPKQKNDPPSLVAKAQLSPSQPVGTFTSPLTTSQKSLRTAPATGQLPGRSS 347
QY 292 POREPQ-----VSHEQFRAALQLVVDGDPDRSYL 321
Db 348 PAGESPRTWHAQISTSNLYLPQDPTVAKGALAGEDTGVVTHEQFKAALRMVQGDPRLL 407
QY 322 DNFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYOHENNVBM 381
Db 408 DSYVWVIGSGSTGIVCLAREKHSGRQVAVKMDLRKQORRELLFNEVIMRDYOHENNVBM 467
QY 382 YNSYLVGDELWVMEFLEGGALTDIVTHTRMNEBQIAAVCLAVLQALSVLHAQGVHRI 441
Db 468 YKSYLVGBELWVMEFLEGGALTDIVSQVRLNEEQIATVCEAVLQALAYLHAQGVHRI 527
QY 442 KSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSILVGTPTYWMAPELISRLPYGPEVDIWSL 501
Db 528 KSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSILVGTPTYWMAPEVIRSLEYATEVDIWSL 587
QY 502 GIMVIMVDGPPYFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFIDRLVDRPAQRA 561
Db 588 GIMVIMVDGPPYFSDSPQAMKRLDSDPPKLNKSHKVSPLVDRFLERMLVDRPOERA 647
QY 562 TAAELLKHPFLAKAGPPASIVPLMRQNR 589
Db 648 TAAELLKHPFLKQTGLPECLVPLIQLYR 675

RESULT 8

US-09-291-417D-29
; Sequence 29, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329

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; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 681
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-291-417D-29

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[illegible]

RESULT 9
US-09-765-815-2
; Sequence 2, Application US/09765815
; Patent No. 6673586
; GENERAL INFORMATION:
; APPLICANT: Balk, Steven
; TITLE OF INVENTION: NO. 6673586el Steroid Hormone Receptor
; TITLE OF INVENTION: Interacting Protein Kinase

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; FILE REFERENCE: 01948/068002
; CURRENT APPLICATION NUMBER: US/09/765,815
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/176,859
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: fastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-765-815-2

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Query Match	47.6%	Score 1470.5	DB 4	Length 681
Best Local Similarity	48.0%	Pred. No. 4.8e-87		
Matches 330; Conservative	70	Mismatches 169	Indels 119	Gaps 12
QY	4	KRKRVEISAPSNFHRVHTGFGDQEOKEFTGLDPRQMSLIEESARRPKPLVDPACITSIQ	63	
Db				
QY	5	KKKRPEISAPQNFQHKRVHTSFDPKGKFFVLGFPQWQNIL-DTLRRKPPVVDPSRITRVQ	63	
Db				
QY	64	PGAPKTTVRGSKGAKGALITLLDEFENMSVTRSNLRSDRSPPPPAR	112	
Db				
QY	64	LQPMKTVVRGSAVPDGYISGLLNDIQKLSVISNTLGRSPTSRRAQSLGGLGDEHWA	123	
Db				
QY	113	-----QNGM-----PEEPATTARGGPKAGSRG-	135	
Db				
QY	124	TDPMYLQSPQSERTDPHGLYLSGNGTTPAGHKOMPWPEQPSPVLVPLNGLAAKAQSLGPA	183	
Db				
QY	137	RFAGHSEAG--GGSGDRRRAGPEKRPKSGREGSGGQESSRDKRPLS-	183	
Db				
QY	184	EFQASQRCLQGLACLOSSPPGASPPGTGTRNHGMKAAKHGSEEARPOSCLVGSATGPPG	243	
Db				
QY	184	DVGTPTPAGLASGAKLAAGRPNTYPRADTDHPGSRGAQGFPHDVAPNGSPSAGGLAIPOSS	243	
Db				
QY	244	E-GSPSPKTRRESSLKRLLFRSM-PLSTAATAAPPSSSKPGPPQSPKPN-----	288	
Db				
QY	244	SSSRPP-----TRRAGAPSP---GVLGPHASEPQLAPPACTPAAPVAPGPPGERS	291	
Db				
QY	289	-SSFRPPQKONPPSLVAKAOSLPDQPVGTFPSPLTTSPTSQSKSLRTATATGQLPGRSS	347	
Db				
QY	292	QREPOR-----VSHEQFPAALQLVVDPCGDRSYL	321	
Db				
QY	348	PAGSPRTWHAQISTSNLYLPQDPPTVAKAALAGEDTGVVTHEQFKAALRMVVVDQGDPRLLL	407	
Db				
QY	322	DNFTKIGEGSTGIVCIATVRSSGKLVAKXMDLRFKQORRELLFNEVVMIRDYQHENVNEM	381	
Db				
QY	408	DSYVKIGEGSTGIVCLAREXHSQVAVKXMDLRFKQORRELLFNEVVMIRDYQHENVNEM	467	
Db				
QY	382	YNSYLVGDGLVVMVMEFLGGALTDIVTHTRMNERQIIAAVCLAVLQALSVLHAQGVIRHDI	441	
Db				
QY	468	YKNYLVGEELVWLMEFLQGGALTDIVSQVRLNEEQIATVCEAVLQALVLAHLHAQGVIRHDI	527	
Db				
QY	442	KSDSILLTHDGRVKLSDFGFCVAVSKVBRKSLVGTGPYMWAPELISRLPYGPEVDIWSL	501	
Db				
QY	528	KSDSILLTLDRGVKLSDFGFCVAVSKVBRKSLVGTGPYMWAPELISRLPYGPEVDIWSL	587	
Db				
QY	502	GIMVIEWVDEGPPYFNBPPLKAMKWRIDNLPPLRLKTLHKVSPSLKGFGLRLLVDRDPQRA	561	
Db				
QY	588	GIMVIEWVDEGPPYFSDSPVQAMKELRDSPPPKLKNSHKSVPLRDLFLERMLVRDPQERA	647	
Db				
QY	562	TAABELLKHPFLAKAGPPASIVPLMRQNR	589	
Db				
QY	648	TAOELLDPHFLLOTGLPECLVPLITOLYR	675	
Db				

RESULT 10
US-09-082-737-3
; Sequence 3, Application US/09082737
; Patent No. 6013500
; GENERAL INFORMATION:
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4; A No. 6013500el Gene Encoding A Serine/

; TITLE OF INVENTION: Threonine Kinase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11230
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,737
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/55311
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-082-737-3

Query Match 41.3%; Score 1277; DB 3; Length 250;
Best Local Similarity 99.6%; Pred. No. 4.5e-75;
Matches 249; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 324 FIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVVMRDYQHENVVMYN 383
Db 1 FIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVVMRDYQHENVVMYN 60

QY 384 SYLVGDELWVMVEFLEGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHSDIKS 443
Db 61 SYLVGDELWVMVEFLEGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHSDIKS 120

QY 444 DSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLGI 503
Db 121 DSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLGI 180

QY 504 MVIEMVDGEPYPFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFLLVDRDPQARATA 563
Db 181 MVIEMVDGEPYPFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFLLVDRDPQARATA 240

QY 564 AELLKHPFLA 573
Db 241 AELLKHPFLA 250

RESULT 11
US-09-718-032-3
; Sequence 3, Application US/09718032
; Patent No. 6667168
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
; FILE REFERENCE: 575/55311-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/718,032
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11341
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/082,737

; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 250
; TYPE: PRT
; ORGANISM: human
US-09-718-032-3

Query Match 41.3%; Score 1277; DB 4; Length 250;
Best Local Similarity 99.6%; Pred. No. 4.5e-75;
Matches 249; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 324 FIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVVMRDYQHENVVMYN 383
Db 1 FIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVVMRDYQHENVVMYN 60

QY 384 SYLVGDELWVMVEFLEGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHSDIKS 443
Db 61 SYLVGDELWVMVEFLEGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHSDIKS 120

QY 444 DSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLGI 503
Db 121 DSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLGI 180

QY 504 MVIEMVDGEPYPFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFLLVDRDPQARATA 563
Db 181 MVIEMVDGEPYPFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFLLVDRDPQARATA 240

QY 564 AELLKHPFLA 573
Db 241 AELLKHPFLA 250

RESULT 12
US-08-935-760-2
; Sequence 2, Application US/08935760A
; Patent No. 5952217
; GENERAL INFORMATION:
; APPLICANT: Gorman, Jessica A.
; APPLICANT: Manly, Susan
; TITLE OF INVENTION: Recombinant Yeast Cell and Assay Using Same
; FILE REFERENCE: ON0156sequence
; CURRENT APPLICATION NUMBER: US/08/935,760A
; CURRENT FILING DATE: 1997-09-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Rattus exulans
US-08-935-760-2

Query Match 29.5%; Score 912; DB 2; Length 544;
Best Local Similarity 35.7%; Pred. No. 3.3e-51;
Matches 210; Conservative 87; Mismatches 166; Indels 126; Gaps 8;

QY 4 KKKKRVETISAPSNFHRVHTGFDQHEQKFTGLPRQWQSLIE-----ESARRPKPLVDP 56
Db 63 KKKKRVETISAPSNFHRVHTGFDQHEQKFTGLPRQWQSLIE-----ESARRPKPLVDP 121

QY 57 ACITSIQPGAPKTIIVRGSKGAKDGLTLLLDDEFENMVSRTSNLRRDPPPPARARQENG 116
Db 122 -----VLKFYDSKETVNNQKYSFT----- 141

QY 117 MPEBPAITARGPGKAGSRGRFAGHSEAGGSGRRRAGPKRPKSSREGSGGQESSRD 176
Db 142 -----SGDKSAHYIAHQ-----SNTKTASEPPLAPPVSEEDDEEEBDD 184

QY 177 KRPLSGPDVGTPOQAGLASGAKLAAGRPFTNYPRADTDHPSRGAQGEPHDVAPNPSAGG 236
Db 185 NEP-----PVIAPRPHETKS-----IYTRSVESIASPA-----APNKEATPP 223

304 QPKELIINEILLVMENKNPNIVNYLDSYLVGDBELVVMVEYLAGGSITDVVTETCMDVQG 363 Db

417 IAAVCLAVLQALSVLHAQVTHRDIKSDISILLTHDGRVKLSDFGCAQVSKVEPRKSLV 476 QY

364 IAAVCRECLQALDFLHSQVTHRDIKSDNILLGMDGSVKLTDFGCAQITPESKSTWV 423 Db

477 GTPYWMAPELISRLPYGPEVDIWSLIGMIVIEWMDGEPYPNEPPLKAMKIRINLPLRK 536 QY

424 GTPYWMAPEVTRKAYGPKVDIWSLIGMIAEMWEGEPYLNENPLRILYLIATNGTPELQ 483 Db

537 NLHKVSPSLKGFLLRDLVRDPAQRATAELLKHFPFLAKAGGPASIVPLM 585 QY

484 NPERLSAVFHDPLNRCLMDVDRGSAKELLOHFPFLAKPLSSITPLI 532 Db

RESULT 15

US-08-615-942A-2
Sequence 2, Application US/08615942A
Patent No. 5863532
GENERAL INFORMATION:
APPLICANT: JOLINDA A. TRAUGH
APPLICANT: REGINA D. ROONEY
APPLICANT: ROLF JAKOBI
APPLICANT: POLYGENA T. TUAZON
APPLICANT: CHARNG-JUI CHEN
APPLICANT: WILLIAM E. MEER
APPLICANT: EDWARD J. CARROLL, JR.
APPLICANT: CURTIS A. MONNIG
TITLE OF INVENTION: Compositions and Methods Comprising
TITLE OF INVENTION: Cytostatic Protein Kinase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa St., Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/615.942A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NONE
FILING DATE: NONE
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Wong, Wean K.
REGISTRATION NUMBER: 33,561
REFERENCE/DOCKET NUMBER: 1279-203XX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213/977-1001
TELEFAX: 213/977-1003
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 524 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-615-942A-2

Qy	4	KRKRKVBISAPSNEFEHVHTGFDQHOEQKFTGLPQWQSLIE-----ESARRRPRLVDP	56
Db	67	KEKERPEISPPSPDEHTIHVGFDVATGEBTGMPQWARLLQTSNITKLEQKKNPOAVLD-	125
Qy	57	ACITSIQGAPKTVIRGSKGAKOGALTLLDEFENMVSVTRSNLRFD--SPPPPARAQE	114
Db	126	-----VLKPYD-----SNTVKQKYLSTFP-----EK	147
Qy	115	NGMPEEPATTARGGPGKAGSRGRFAGHSEAGGGSGDRRRRAGPEKRPKPSRSGSGQPBS	174
Db	148	DGRFS-----GAPALNTKVSETSAVVTEEDD	173
Qy	175	RDKRPLSGPDVGTPOPAGLASGAKLAAGRPEYTPRADTDHPSRGAQGEHPHDVAFNP	234
Db	174	DDEE--AAPPVIAIRPDHTKS-----IYTRSVID-FIPAPVGDSH-----	210
Qy	235	GGLAIPOSSSSSRPPTRARGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGPRSP	294
Db	211	-----VDSGAKSSDK-----QK	222
Qy	295	EPQRVSHQFRAALQLVDPGDPRSRYLDNFTKIGEGSTGIVCIATVRSGKLVAVKMDL	354
Db	223	KTKNTDEETMEKLRITVSGIDPKKKVTRYEKIQGASGTVFTATDVALGOEVAIKQNL	282
Qy	355	RKQORRELLNEVVIMRDYQHENVVEMVNSYLVGDELWVMFELEGGALTIDIVTHRXNE	414
Db	283	QKQPKRELTINEILLWELKNPNINVLNLSYLVGDELFWVMXYLAGGSLTDVVVETCME	342
Qy	415	EQIAAACLVIQALSVLHAQVHIRDKSDTILTHDGRVKLSDFGCAQVSKEVPRRKS	474
Db	343	AQIAAACECLQALEFTHANQVHIRDKSDNVLLGMEGSVKLITDFGCAQIITPEQSKRST	402
Qy	475	LVGTPYMABELISRLPYGPEVDIWSIGIMVIEVMVDGEPYPFNEEPLKAMKIRNLDPR	534
Db	403	MVGTPYMAPEVTVTKAYGPKVDIWSLGIAMAIEMVVEGEPYPINENPLRXYLIATNGTPE	462
Qy	535	LKNLHKVSPSLKGFLDRLLVRDPAQRATAAELLKHPPFLAKAGPPASIVPL-----NRQ	587
Db	463	LQNEKLSPIPRDFLNRCLMDWVEKRGSAKELLQHPFLKLAPLSSLTPLINAAEKMS	522
Qy	588	NR	589
Db	523	NR	524

Search completed: September 29, 2004, 18:06:35
Job time : 49.8485 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 17:38:51 ; Search time 16.5132 Seconds
(without alignments)
1863.563 Million cell updates/sec

Title: US-10-693-367-2

Perfect score: 3090

Sequence: 1 MFGRKRKVEISAPNSFEHR.....LAKAGPPASIVPLMRQNR 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3090	100.0	591	PAK4_HUMAN	O96013 homo sapien
2	1731	56.0	719	PAK7_HUMAN	Q9P286 homo sapien
3	1473.5	47.7	681	PAK6_HUMAN	Q9NQU5 homo sapien
4	917	29.7	544	PAK3_RAT	O62829 rattus norv
5	909	29.4	544	PAK3_HUMAN	O75914 homo sapien
6	907	29.4	544	PAK3_MOUSE	Q61036 mus musculu
7	904	29.3	524	PAK2_HUMAN	Q13177 homo sapien
8	900	29.1	524	PAK2_RABIT	Q29502 oryctolagus
9	895	29.0	524	PAK2_RAT	O64303 rattus norv
10	894	28.9	544	PAK1_RAT	P35465 rattus norv
11	892.5	28.9	545	PAK1_HUMAN	Q13153 homo sapien
12	889.5	28.8	545	PAK1_MOUSE	O88643 mus musculu
13	846.5	27.4	1230	ST20_CANAL	Q92212 candida alb
14	837	27.1	939	ST20_YEAST	Q03497 saccharomyc
15	823.5	26.7	658	PAK1_SCHPO	P50527 schizosacch
16	810	26.2	971	CLA4_CANAL	O14427 candida alb
17	760	24.6	842	CLA4_YEAST	P48562 saccharomyc
18	697	22.6	589	SHK2_SCHPO	Q10056 schizosacch
19	651.5	21.1	655	SKM1_YEAST	Q12469 saccharomyc
20	520	16.8	491	STK3_HUMAN	Q13188 homo sapien
21	512.5	16.6	487	STK4_HUMAN	Q13043 homo sapien
22	509.5	16.5	553	SPAK_RAT	O88506 rattus norv
23	498	16.1	471	SID1_SCHPO	O14305 schizosacch
24	497.5	16.1	556	SPAK_MOUSE	Q9Z1W9 mus musculu
25	497	16.0	894	PAK3_HUMAN	Q81VH8 homo sapien
26	495.5	16.0	547	SPAK_HUMAN	Q9UEW8 homo sapien
27	494	16.0	862	M4K3_RAT	Q92412 rattus norv
28	487.5	15.8	916	TNIK_MOUSE	P83510 mus musculu
29	487.5	15.8	1360	TNIK_HUMAN	O9UK55 homo sapien
30	486	15.7	821	M4K2_MOUSE	Q61161 mus musculu
31	484.5	15.7	443	ST24_HUMAN	Q9Y660 homo sapien
32	484	15.7	833	M4K1_HUMAN	Q92918 homo sapien
33	478	15.5	669	HPO_DROME	O8T086 drosophila

RESULT 1

ID	PAK4_HUMAN	STANDARD;	PRT;	591 AA.
AC	O96013; Q9BUJ3;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Serine/threonine-protein kinase PAK 4 (EC 2.7.1.-) (p21-activated kinase 4) (PAK-4).			
DE	kinase 4) (PAK-4).			
GN	PAK4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RN	SEQUENCE FROM N.A. (ISOFORM 1).			
RP	MEDLINE=99043860; PubMed=9822598;			
RX	ABO A., Qu J., Cammarano M.S., Dan C., Fritsch A., Baud V.,			
RA	Belisle B., Minden A.;			
RA	"PAK4, a novel effector for Cdc42Hs, is implicated in the			
RT	reorganization of the actin cytoskeleton and in the formation of			
RT	filopodia".;			
RL	EMBO J. 17:6527-6540(1998).			
[2]				
RN	SEQUENCE FROM N.A. (ISOFORM 1).			
RP	Melnick M.B.;			
RA	Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.			
RL				
RN	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TISSUE=Eye, Pancreas, and Placenta;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,			
RT	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length			
RL	human and mouse cDNA sequences".;			
RL	Proc. Natl Acad Sci U.S.A. 99:16899-16903(2002).			
CC	-!- FUNCTION: ACTIVATES THE JNK PATHWAY. IMPLICATED IN THE			
CC	REORGANIZATION OF THE ACTIN CYTOSKELETON AND IN THE FORMATION OF			
CC	FILOPODIA.			
CC	-!- SUBUNIT: INTERACTS TIGHTLY WITH RAC1.			
CC	CC CDC42/P21 AND WEAKLY WITH RAC1.			

Q9im52 mus musculu
Q12851 h mitogen-a
Q8n4c8 homo sapien
Q95819 homo sapien
Q9y4k4 homo sapien
Q8bpm2 mus musculu
Q00506 homo sapien
Q9z2w1 mus musculu
P70218 mus musculu
O55098 mus musculu
P38692 saccharomyc
P97820 mus musculu

ALIGNMENTS

RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Franks J.A., Fraser A., French L., Garner P.,
 RA Grahnam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leivaeslatho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLeay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund K., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 CC -!- FUNCTION: The activated kinase acts on a variety of targets (By
 CC similarity).
 CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
 CC CDC42/P21 AND RAC1 (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in brain.
 CC -!- PTM: Autophosphorylated when activated by CDC42/p21 (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
 CC STE20 subfamily.
 CC -!- SIMILARITY: Contains 1 CRIB domain.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB040812; BA941194.1; -;
 DR EMBL; AB033090; BA86578.1; ALT_INIT.
 DR EMBL; AL353612; CAC34367.1; -;
 DR HSSP; P24941; 1BUH.
 DR Genew; HGNC:15916; PAK7.
 DR MIM; 608038; -;
 DR InterPro; IPR000095; PAKbox/RhoBndng.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_Thr_pkin_AS.
 DR InterPro; IPR002290; Ser_Thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS01018; CRIB; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 11 24 CRIB.
 FT DOMAIN 25 448 LINKER.
 FT DOMAIN 449 700 PROTEIN_KINASE.
 FT NP_BIND 455 463 ATP (BY SIMILARITY).
 FT BINDING 478 478 ATP (BY SIMILARITY).
 FT ACT_SITE 568 568 BY SIMILARITY.
 SQ SEQUENCE 719 AA; 80744 MW; 07A12B1EBC4E2A02 CRC64;

Query Match 56.0%; Score 1731; DB 1; Length 719;
 Best Local Similarity 52.4%; Pred No. 2,1e-59;
 Matches 393; Conservative 66; Mismatches 126; Indels 156; Gaps 17;
 QY 1 MFGRKKRVEISAPGNFHRVHTGPDQHEQKFTGLPRQWOLIESARPKPLVDPACT 60
 DB 1 MFGRKKKIEISGPNFHRVHTGPDQEQKFTGLPQWHSLLADTANRPKMVDPCIT 60
 QY 61 STOPGAPKTIIVRGSKGAKGALTLLIDPENMVSRTSLRSDSPPPARA-----R 112
 DB 61 PQLAPMKTIVRGKPKCKETSINGLLEDFDNISVTRSLRKSPPPTDQGASSHPGHA 120
 QY 113 QNNGM-----PEEPATTA-----RGG-----PGKA 132
 DB 121 EENGPIITSQYSSESDTTADYTEKYREKSLYGDLDLPYRGSHAAKQNGHVMKMHGEA 180
 QY 133 -----GSRGRFAGH-----SEAG 145
 DB 181 YYSEVKPLKSDFAFSAHYHSHLDSLKPSEYDLKWEYQRASSSSSLDYSEFTPSRTA 240
 QY 146 GSGDERRA-----GP-----EKRPKSREGSGGPOESSRDKPLSGPDVGTP-QPA 191
 DB 241 GTSGGCKSLAYSESEWGPSLDDYDRRPKSSVYNQTSPOPTMR-QKRSRSGSLQPEMPMF 299
 QY 192 GLASGAKLAAGRPFNITY-----PRADTDH-----PSRGAQGEHVDVAPNGP 232
 DB 300 GASAFKTHPQGHYSNITYTYPLSEPTMCIPKVDYDRAQMVLSPLSGS-----DTYPRGP 354
 QY 233 SAGGLAIPOS-----SSSSSRPPTRARGAPSPGLGPHASEPQLAPPACTP----- 278
 DB 355 A-----KLPOSQSKSGYSSSSHQVPSGYHKA-----TLYHHPSLQSSQYISTASYLSLSL 406
 QY 279 AAPAVPGPGPRSPQEPORVSHQEPRAALQLVVDGDPSPSYLDNFIKIGEGSTGIVCIA 338
 DB 407 SSSTYPPPSGSSSDQSPSRVSHQEPRAALQLVVDGDPSPREYLANFIKIGEGSTGIVCIA 466
 QY 339 TVRSSKGLVAVKMDLRKQORRELLFNVEVIMRDYQHENNVEMNSYLVGDELWVWMEFL 398
 DB 467 TEKHTGQVAVKMDLRKQORRELLFNVEVIMRDYHHDNVDMYSSYLVGDELWVWMEFL 526
 QY 399 EGGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHAGQVTHROIKSDSILLTHDGRVKLSD 458
 DB 527 EGGALTDIVTHTRMNEEQIATVCLSVLRALSVLHNGVTHROIKSDSILLTSDGRKLSD 586
 QY 459 FGFCQVSKVEVPKRSKLVGTPTWMAPELISRLPYGPEVDIWSLGIWIMVWDGEPPEYNE 518
 DB 587 FGFCQVSKVEVPKRSKLVGTPTWMAPEVLSRLPYGTEVDIWSLGIWIMVWDGEPPEYNE 646
 QY 519 PPLKAMKMRDMLPPRLKNLHKVSPSLKGLFLDLVLRDPAQRATAAELLKHPFLAKAGPP 578
 DB 647 PPLQAMRIRDSLPVRVKDLHKVSVLRGFLDLMLVLRPSQRATAQELLGHPFLKLAGPP 706
 QY 579 ASIVPLMRQNR 589
 DB 707 SCIVPLMRQVR 717
 RESULT 3
 PAK6_HUMAN
 ID PAK6_HUMAN STANDARD; PRT; 681 AA.
 AC Q9NQU5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Serine/threonine-protein kinase PAK 6 (EC 2.7.1.-) (p21-activated
 DE kinase 6) (PAK-6) (PAK-5).
 GN PAK6 OR PAK5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

DR	PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR	PROSITE; PS00108; PROTEIN KINASE ST; FALSE NEG.
KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.
FT	DOMAIN 12 25 CRIB.
FT	DOMAIN 26 406 LINKER.
FT	DOMAIN 407 658 PROTEIN KINASE.
FT	NP BIND 413 421 ATP (BY SIMILARITY).
FT	BINDING 436 436 ATP (BY SIMILARITY).
FT	ACT SITE 526 526 BY SIMILARITY.
SQ	SEQUENCE 681 AA; 74868 MW; P20A4FA257649BB9 CRC64;

Query Match		47.7%; Score 1473.5; DB 1; Length 681;
Best Local Similarity		48.1%; Pred. No. 1.1e-49;
Matches 331; Conservative		69; Mismatches 169; Indels 119; Gaps 12;

Qy	4	KRKRVEISAPSNFHRVHTGFDGHEOKFTGLPRMQSLIEESARRPKPLVDPACTISIQ	63
Dd	5	KKKRRPEISAPNQFQRVHVSFDPEKEGFGVLPPQWNIL-DTLRRPKPVDPSSRIIRVQ	63
Qy	64	PGAPKTIIVRGSKAKDGALITLLDEFENMGSVTRNSLRDSDPPPAPAR	112
Dd	64	LQPMKTIVRGSAAMPVDGYISGLLNDIOKLSVISNTLRGRSPTSGRRRAQSLLGLGDHWA	123
Qy	113	-----QBNGM-----PEEPATTARGGPKAGSRG-	136
Dd	124	TDDPMYLQSQSBRTDPHGHIYLSNCGTTPAGHKOMPPEQSPFRVLNGLAAKAQSLGPA	183
Qy	137	RFAHGEAG---GGSGDRLRAGPEKRPKSREGSGGQESSRDKRPLS-----GP	183
Dd	184	EFGASQRCLQGACIQLQSSPPGASPTGTNRHGMAAKAHGSEARPQSCLVGSATGRP	243
Qy	184	DVGTPOAGLASGAKLAAGRPFNTYPADTDHPSRGAQGHVDVAPNGPSAGGLAI PQSS	243
Dd	244	E-GSPGPKTRESSLKRLRFRSM-FLSTAAAPPSSSKGPPPPQSKPN-----	288
Qy	244	SSSSRPP-----TRARGASP--GVLGPHASEPQLAPPACTPAAPAVPGPPGPRS	291
Dd	289	-SSFRPPQKNPSPSLVAKAQSLFSQPVGTFPLTTSDTSPPQSKSLRTATPATGOLPGRSS	347
Qy	292	PQREPOR-----VSHQFPAAALQLVDPGDPDSYL	321
Dd	348	PAGSPRTWHQAISTSNLYLPQDPTVAKGALAGEDTVGVTHQFKAALRMVWDQDPRLLL	407
Qy	322	DNFIKI GEGSTGIVCIATVRSSGKLVAVKMDLTKQORRELLFNFEVMIDYQHENVVEM	381
Dd	408	DSYVKIGESTGIVCLAREKHSGRVAVKMDLTKQORRELLFNFEVMIDYQHENVVEM	467
Qy	382	YNLYVGDELWVMEFLEGGALTDIVTHTRMBEQIAAVCLAVIALSVLHAQGVIHEDI	441
Dd	468	YKSYLVGEELWLWMEFLQGGALLDIVSQVRNLBEQIATVCVEAVLQALAYLHAQGVIHEDI	527
Qy	442	KDSPILLTDGRVKLSDGFCAOVSKVEVPKRSIVGTPIYMWAPELLISRLPYGPEVDIWSL	501
Dd	528	KDSIIULLDGRVKLSDGFCAQISKDVPKRSKLVGTPYMWAEPIVSRSIYATEVDIWSL	587
Qy	502	GIMVIEMVDGEPFYNEPPLKAMKMRINDLNPPRLKMLHKVSPSLKGFLDLLVRDPAQRA	561
Dd	588	GIMVIEMVDGEPFYFSDSPVOAMKRLRSDSPPKIKNSHKVSPVLDFLERMLVRDPOERA	647
Qy	562	TARELLKHPELAKAGPPASTIVPLMRQNR	589
Dd	648	TAOELLDHBPFLLTQTGLPECLVPLIQLYR	675

RESULT 4	
ID_PAK3_RAT	STANDARD; PRG; 544 AA.
AC_QG2829;	
DT_01-NOV-1997 (Rel. 35, Created)	
DT_01-NOV-1997 (Rel. 35, Last sequence update)	
DT_28-FEB-2003 (Rel. 41, Last annotation update)	
DE_Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-) (p21-activated	

DE kinase 3) (PAK-3) (Beta-PAK) (P65-PAK).
GN PAK3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE OF 37-56.
RC TISSUE=Brain;
RX MEDLINE=96027610; PubMed=7559638;
RA Manser E., Chong C., Zhao Z.-S., Leung T., Michael G., Hall C.,
RA Lim L.;
RT "Molecular cloning of a new member of the p21-Cdc42/Rac-activated
RT kinase (PAK) family.";
RL J. Biol. Chem. 270:25070-25078(1995).
CC -!- FUNCTION: The activated kinase acts on a variety of targets.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3
CC DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK (BY
CC SIMILARITY).
CC -!- TISSUE SPECIFICITY: DETECTED AT HIGH LEVELS IN THE BRAIN AND AT
CC LOW LEVELS IN THE TESTIS.
CC -!- DEVELOPMENTAL STAGE: FOUND IN THE EMBRYONIC CNS WITH LITTLE
CC EXPRESSION ELSEWHERE.
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U33314; AAC52268.1; -;
DR PIR; A57597; A57597.
DR HSSP; P24941; ICKP.
DR InterPro; IPR000095; PAKbox/Rho-binding.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser thr pkin AS.
DR InterPro; IPR002290; Ser thr pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 70 83 CRIB.
FT DOMAIN 84 267 LINKER.
FT DOMAIN 268 519 PROTEIN KINASE.
FT NF BIND 274 282 ATP (BY SIMILARITY).
FT BINDING 297 297 ATP (BY SIMILARITY).
FT ACT SITE 387 387 BY SIMILARITY.
SQ SEQUENCE 544 AA; 60710 MW; 7B940FC204A2B48B CRC64;

Query Match 29.7%; Score 917; DB 1; Length 544;
Best Local Similarity 35.8%; Pred. No. 1.1e-28;
Matches 211; Conservative 87; Mismatches 165; Indels 126; Gaps 8;

QY 4 KRKRVEISAPSFHEHVHTGFGDHEQKFGTGLPRWQSLIE-----ESARPPELVDP 56
DB 63 KEKERPEISLPSDFEHTIHVGFDAVTGFTGIPEQMARLLQTSNITKLEQKNPQAVLD- 121

QY 57 ACITSIQPGAPKTIVRGSKGAKDGALTLLLDDEFENMSVTRNSLRDSDPPPPARARQENG 116
DB 122 -----VLKPYDSKETVNNQKYSFT----- 141
QY 117 MPEEPATTARGGPGKAGSRGRFAGHSEAGGGDRRRAGPEKRPKSSREGSGPGQSSRD 176
DB 142 -----SGDKSAHYIAAHQ-----SNTKTASEPPLAPPVSEDEDEEEEDD 184
QY 177 KPPLSGPDVGTQPGAGLAKAGRPNTYPRADTDHPSRCAQGEPHDVAENGPSAGG 236
DB 185 NEP---PPVIAPRPETHKS-----IYTRSVESIASPA-----APNKKEATPP 223
QY 237 LAIPQSSSSSRPPTRRARGAPSPGLPHASEPOLAPPACTPAAPAVPGPPGSRSPREP 296
DB 224 SLENANSSLYRNTDR----- 243
QY 297 QRVSHQFRAALQLVVDPGDPRSILDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRK 356
DB 244 SKMTDEILEKLRISVSGDPKKKYTRFEKIGOGASGTVTALDIATQGEVAIKQNNLQ 303
QY 357 QQRRELLFNEVIMRDYOHENVVEMVNSVLGDELWVMEFLEGGALTDIVVTHRNNEEQ 416
DB 304 QPKELIINEILLVMRENKPNINYLDSVLGDELWVMEYLAGGSLTDVVTETCDEGQ 363
QY 417 IAAVCLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLV 476
DB 364 IAAVCRECLQALDFLHNSQVHHRDIKSDNILLGMDGSKVLTDFGCAQITPEOSKSTMV 423
QY 477 GTPYMAPELIRLPYGPVEVDIWSLGMVIMVVDGPPYFNEPPLKAMKIRDLNPPRLK 536
DB 424 GTPYMAPEVTVTKAYGPKVDIWSLGMALMEVGEPPVLYNENPLRALYLIATNGTPELQ 483
QY 537 NLHKVSPSLKGLDRLLDVDPQQRATAAELLKHFFLAKAGPPASIVPLM 585
DB 484 NPERLSAVFRDFLNRCLMDVDVRRGSAKELLQHPFLKLAKPLSSLPLI 532

RESULT 5
PAK3 HUMAN STANDARD; PRT; 544 AA.
ID PAK3_HUMAN
AC 075914;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-) (p21-activated
DE kinase 3) (PAK-3) (Beta-PAK) (Oligophrenin-3).
GN PAK3 OR OPHN3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND DISEASE.
RX MEDLINE=98400251; PubMed=9731525;
RA Allen K.M., Gleeson J.G., Bagrodia S., Partington M.W.,
RA Macmillan J.C., Cerione R.A., Mulley J.C., Walsh C.A.;
RT "PAK3 mutation in nonsyndromic X-linked mental retardation.";
RL Nat. Genet. 20:25-30(1998).
CC -!- FUNCTION: The activated kinase acts on a variety of targets.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3
CC DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN POSTMITOTIC NEURONS OF THE
CC DEVELOPING AND POSTNATAL CEREBRAL CORTEX AND HIPPOCAMPUS.
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- DISEASE: Defects in PAK3 are the cause of non-specific X-linked
CC nonsyndromic mental retardation type 30 (MRX30) [MIM:300142].
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC
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CC or send an email to license@isb-sib.ch).

DR EMBL; AF068864; AAC36097.1; --
DR HSSP; P24941; 1CKP.
DR Genew; HGNC:8592; PAK3.
DR MIM; 300142; --
DR InterPro; IPR000095; PAKbox/RhoBndng.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00669; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW SH3-binding; Phosphorylation. CRIB.
FT DOMAIN 70 83
FT DOMAIN 84 267
FT LINKER.
FT DOMAIN 268 519
FT PROTEIN_KINASE.
FT NP_BIND 274 282
FT ATP (BY SIMILARITY).
FT BINDING 297 297
FT ATP (BY SIMILARITY).
FT ACT_SITE 387 387
FT BY SIMILARITY.
SQ SEQUENCE 544 AA; 60692 MW; 230AF6952CB049E2 CRC64;

Query Match 29.4%; Score 909; DB 1; Length 544;

Best Local Similarity 35.0%; Pred. No. 2.2e-28;

Matches 206; Conservative 89; Mismatches 168; Indels 126; Gaps 8;

QY 4 KRKKVEISAPSNFHRVHTGFDQHEQKFTGPRWOSLIE-----ESARRKPLVDP 56
DB KEKEPEISLPDFEHTIHVGFDVATGFTGIPQWARLLQTSNITKLEQKNPQAVLD- 121
QY 57 ACITSIQGPAPKTIVRGSKAGDGAULTLLDLDEFNMSTVRSNLSLRDSSPPPARQENG 116
DB -----VLKPYDSKETVNNQYMSFT----- 141
QY 117 MPEEPATTARGPGKAGSRGRFAGHSEAGGSGDRRRAGPEKRPKSSRGGSGPQESSRD 176
DB -----SGDKSAHGTYAAHP-----SSTKTASEPPLAPPVSEEDDEEEDEE 184
QY 177 KRPLSGPDVGTQPPAGLASGAKLAAGRPNPTVPRADTDHPSRGAQGEHPDVAPNGPSAGG 236
DB 185 NEP-----PPVIAPRPHTKS-----IYRSVVE----- 208
QY 237 LAIQSSSSSSPPTTRAGAPSGVLGPHASEPQAPPACTPAAPAVPGPGPRSPQREP 296
DB -----SIASPAVPNKEVTPPSAENANSSTLYRNTDR--QRKK 243
QY 297 QRVSHQEPFAALQVLVDPGDPSYLDNFKIGEGSTGIVCIATVRSSGKLVAVKMDLRK 356
DB SMTDDEETLEKLRSVSGDPPKKYTRFEKIQGASGVTVYALDITATGQEVAKQNNLQQ 303
QY 357 QRRRELLFNVEIMRDYQHENVVMYNSYLVDGLVWVMEFLGGALTDIVTHTRNBEQ 416
DB QPKCELLINEILLVMRENKPNIVNLYDSVLVDGLVWVMEYLAGSLTDVVTETCNDCEQ 363
QY 417 IAAVCLAVIQAQSVLHAQGVTHRDITKSDSILITHDGRVKLSDFGCAQVSKVEVPRKSLV 476
DB IAAVCRECLQALDFLHNSQVTHRDITKSDNILLGMDGSKVLTDGFCQAQITPEQSKRSTWV 423
QY 477 GTPYWMAPELISLPLPGPEVDWISLGIWVIEWDCGPPYFNEPPLKAMKMWIRNLPPLK 536
DB ----- 536

DB 424 GTPYWMAPVTRKAYGPKVDITWSLGIWVIEWDCGPPYFNEPPLRALLYLIATNGTPELQ 483
QY 537 NLHKVSPSLKGLDRLVDRDPAQRATAAELLKHPLAKAGPPASIVPLM 585
DB 484 NPERLSAVFRDFLNRKCLEMDVDRRGSAKELLQHPFLKLAFLUSLTPLI 532

RESULT 6

PAK3 MOUSE
ID PAK3 MOUSE STANDARD; PRT; 544 AA.
AC Q61036; O88645;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-) (p21-activated
DE kinase 3) (PAK-3) (Beta-PAK) (CDC42/RAC effector kinase PAK-B).
GN PAK3 OR PAK-3 OR STK4 OR PAKB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE=Fibroblast;
RX MEDLINE=96032693; PubMed=7559398;
RA Bagrodia S., Taylor S.J., Creasy C.L., Chernoff J., Cerione R.A.;
RT "Identification of a mouse p21Cdc42/Rac activated kinase.";
RL J. Biol. Chem. 270:22731-22737(1995).
RN [2]
RP ERRATUM.
RA Bagrodia S., Taylor S.J., Creasy C.L., Chernoff J., Cerione R.A.;
RL J. Biol. Chem. 271:1250-1250(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99282526; PubMed=10352232;
RA Burdello P.D., Kozak C.A., Finegold A.A., Hall A., Piore D.M.;
RT "Cloning, central nervous system expression and chromosomal mapping of
RT the mouse PAK-1 and PAK-3 genes.";
RL Gene 232:209-215(1999).
CC -!- FUNCTION: The activated kinase acts on a variety of targets.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND.
CC CD42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3
CC DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK.
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC ST20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC
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CC or send an email to license@isb-sib.ch).

EMBL; U39738; AAC52354.1; --
DR EMBL; AF082297; AAC31969.1; --
DR PIR; I49376; I49376.
DR PDB; 1EES; 12-APR-00.
DR MGI; MGI:1339656; PAK3.
DR InterPro; IPR000095; PAKbox/RhoBndng.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00669; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS0108; CRIB; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW SH3-binding; Phosphorylation; 3D-structure.
FT DOMAIN 70 83 CRIB.
FT DOMAIN 84 267 LINKER.
FT DOMAIN 268 519 PROTEIN KINASE.
FT NP_BIND 274 282 ATP (BY SIMILARITY).
FT BINDING 297 297 ATP (BY SIMILARITY).
FT ACT_SITE 387 387 BY SIMILARITY.
FT CONFLICT 161 161 G -> A (IN REF. 3).
FT CONFLICT 361 361 V -> E (IN REF. 3).
FT CONFLICT 493 493 H -> R (IN REF. 3).
FT CONFLICT 525 525 L -> M (IN REF. 3).
SQ SEQUENCE 544 AA; 60683 MW; C4AE871DD33E6988 CRC64;

Query Match 29.4%; Score 907; DB 1; Length 544;
Best Local Similarity 34.6%; Pred. No. 2.6e-28;
Matches 204; Conservative 90; Mismatches 169; Indels 126; Gaps 7;

QY 4 KRKRVEISAPSNFHRVHTGFQHQKFTGLPRQWSLIE-----ESARRPKPLVDP 56
DB 63 KEKERPEISLPSDFEHTIHVGFDAVTEGTGIPQWARLLQTSNITKLEQKKNPQAVLD- 121
QY 57 ACITSIQPGAPKTIIVRGSKAGDKGALTLTLLDEPENMSVTRNSLRRDSPPPPARARQENG 116
DB 122 -----VLKFDYSKETVNNQKMSFT----- 141
QY 117 MPEEPATTARGPGKAGSRGRFAGHSEAGGGSDRRRAGPERKPKSRSGSGQPQSSRD 176
DB 142 -----SGDKSAHGYYIAHQ-----SNTKTGSEPPPLAPPVSEEEDEEEEDD 184
QY 177 KRPLSGPDVGTPOGASAKLAAGRPNTYPRATDTPSRCAQGEPHDVAENGSAAG 236
DB 185 NEP---PPVIAPRPEHTKS-----IYTRSVVESIASPAAPNKEDIPPSAENANS 230
QY 237 LAIPQSSSSSSRPPTTRARGAPSPGLVGHASEPQLAPPACTPAAPVPGPPGPRSPQRE 296
DB 231 TLYRYNTDR-----QRKK 243
QY 297 QRVSHEQFRAALQLVDPDGPDSYLDNFIKIGBSTGIVCIATVRSSGKLVAVKKMDLRK 356
DB 244 SKMTDEILLEKLRISVSGDPKKYTRLEKIGQASGVTVTALDIATQGEVAIKQWNLQ 303
QY 357 QQRRELLFNEVIMRDYQHENVEMVNSYLVGDELWVMEFLEGGALTDIVHTRNNEQ 416
DB 304 QPKKELIINEILVMRENKPNINYLDSYLVGDELWVMEYLAGSGLTDVVTETCDVVG 363
QY 417 IAAVCLAVLQALSVLHAQGVHHRDIKSDSITLLTHDGRVKLSDFGCAQVSKVEPRKSLV 476
DB 364 IAAVCRECLQALDFLHNSQVHHRDIKSDNILLGMDSVKLTDFGCAQITPEQSKRSTW 423
QY 477 GTPYMWAPELISRLPYGPEVDIWSLGIWVMDGPEPPYFNEPPLKAMKMRDNLPPRLK 536
DB 424 GTPYMWAPVETRKAYGPKVDIWSLGIWVMDGPEPPYFNEPPLKAMKMRDNLPPRLK 536
QY 537 NLHKVSPSLKGLFDRLLDVDPQARATAEELKHPFLAKGPPASIVPLM 585
DB 484 NPERLSAVFDFLNRCLMDVDRRGSAKELLQHPFLKAKPLSLTFLI 532

RESULT 7
ID_PAK2_HUMAN STANDARD; PRT; 524 AA.
AC Q13177; Q13154;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase PAK 2 (EC 2.7.1.1-) (p21-activated
DE Kinase 2) (PAK-2) (Gamma-PAK) (S6/H4 kinase).
GN PAK2.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sells M., Knause U.J., Bagrodia S., Ambrose D., Bokoch G.M.,
RA Chernoff J.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 32-524 FROM N.A., AND SEQUENCE OF 401-417.
RC TISSUE=Placenta;
RX MEDLINE=953262637; PubMed=7744004;
RA Martin G.A., Bollag G., McCormick F., Abo A.;
RT "A novel serine kinase activated by rac1/CDC42Hs-dependent
RT autophosphorylation is related to PAK65 and STE20.";
RL EMBO J. 14:1970-1978(1995).
RN [3]
RN ERRATUM.
RP MEDLINE=96016211; PubMed=7556080;
RA Martin G.A., Bollag G., McCormick F., Abo A.;
RL EMBO J. 14:4385-4385(1995).
RN [4]
RN AUTOPHOSPHORYLATION.
RX MEDLINE=95403344; PubMed=7673144;
RA Benner G.E., Dennis P.B., Masaracchia R.A.;
RT "Activation of an S6/H4 kinase (PAK 65) from human placenta by
RT intramolecular and intermolecular autophosphorylation.";
RL J. Biol. Chem. 270:21121-21128(1995).
CC -!- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.
CC -!- PHOSPHORYLATES RIBOSOMAL PROTEIN S6, HISTONE H4 AND MYELIN BASIC
CC PROTEIN.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/P21 AND RAC1.
CC -!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED. HIGHER LEVELS SEEN IN
CC SKELETAL MUSCLE, OVARY, THYMUS AND SPLEEN.
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC
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CC
EMBL; U24153; AAA65442.1; -;
DR EMBL; U25975; AAA75468.1; -;
DR PIR; S58682; S58682.
DR HSSP; P24941; ICKP.
DR Genew; HGNC:8591; PAK2.
DR MIM; 605022; -;
DR GO; GO:0004672; F:protein kinase activity; TAS.
DR GO; GO:0006469; P:negative regulation of protein kinase activity; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR000095; PAKbox/RhoBindg.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr pkin AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.

FT DOMAIN 74 87 CRIB.
FT DOMAIN 88 248 LINKER.
FT DOMAIN 249 499 PROTEIN KINASE.
FT NP_BIND 255 263 ATP (BY SIMILARITY).
FT BINDING 278 278 ATP (BY SIMILARITY).
FT ACT_SITE 367 367 BY SIMILARITY.
FT CONFLICT 90 90 A -> T (IN REF. 2).
FT CONFLICT 150 150 L -> P (IN REF. 2).
FT CONFLICT 225 225 P -> T (IN REF. 2).
FT CONFLICT 329 329 G -> R (IN REF. 2).
FT CONFLICT 338 338 T -> TA (IN REF. 1).
SQ SEQUENCE 524 AA; 58004 MW; DB2A7A72BB6B1072 CRC64;

Query Match 29.3%; Score 904; DB 1; Length 524;

Best Local Similarity 35.0%; Pred. No. 3.3e-28;
Matches 211; Conservative 94; Mismatches 136; Indels 162; Gaps 13;

QY 4 KKKRVEISAPSNFHRVHTGFDQHEQKFTGLPROMQSLIE-----ESARRPKPLVDP 56
Db 67 KEKERPEISPPSDFEHTIHVGFDVAVTGFTGMPEQWARLLQTSNITKLEQKNPQAVLD- 125
QY 57 ACITSIQCAPKTIIVRGSKAGDKGALTLLDDFENMSVTRNSLRD--SPPPPARAQE 114
Db 126 -----VLKEYD-----SNTVKQKYLSTFP-----EK 147
QY 115 NGMPE-EPATTARGGPKAGSRGAFHSEAGGSDRRRAGPEKPKSSREGSGGPQES 173
Db 148 DGLPGTGNALNAG-----TEA-----PAVTEEDDDDET 178
QY 174 SDRKPLSGPDVGTQPAGLASGAKLAAGRPNTYPRADTHPSRGAQGEHDPVAPNGPS 233
Db 179 A-----PPVIAPRPDHTKS-----IYTRSVID-PVPAPVGDSh----- 210
QY 234 AGGLAIPOSSSSSRPRTRAGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGRSPQ 293
Db 211 -----VDGAAKSLDKQ 221
QY 294 REPQVSHEQFRAALQLVVDGPRSLDNEFKIGEGSTGIYCIATVRSSGKLVAKKMD 353
Db 222 KKKPKMTDEEINEKURTIVISGDPKKYTRYEKIQGAGSTVFTADVALGQEVAKQIN 281
QY 354 LRQQRRELLFNEVMIRDYQHENVVMSYLVGDELWVMVEFLEGGALTDIVTHRMN 413
Db 282 LQKQPKKELIINEILVMKELKNPNIWNFLDSYLVGDELFWVMYLAGSLTDVVTETMD 341
QY 414 EQQIAVCLAVLQALSVLHAQGVHRIKSDSILLTHDGRVLSDFGCAQVSKVPRRK 473
Db 342 EAQIAAVCRECIQALEFLHANQVHRIKSDNVLGMESGVKLTDFGCAQITPEQSKRS 401
QY 474 SLVGTPTYMAPELISRLPYGPEVDIWSLGIWMIEMVDGEPYFNPPLKAMKWRDNLPP 533
Db 402 TWVGTPTYMAPEVTVTKAKGPKVDIWSLGIWMIEMVEGEPYFNPPLKALYLIATNGTP 461
QY 534 RLKNLHKVSPSLKGFLLRDLVRDPAQRATAELLKHPFLAKAGPPASIVPL-----MR 586
Db 462 ELONPEKLSPIFRDFLNRCLMDVEKRGSAKELLQHPFLKAKPLSLPLIIMAAKEAMK 521
QY 587 QNR 589
Db 522 SNR 524

RESULT 8

PAK2 RABIT
ID PAK2_RABIT STANDARD; PRT; 524 AA.
AC Q29502;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase PAK 2 (EC 2.7.1.-) (p21-activated
kinase 2) (PAK-2) (Gamma-PAK) (p21-activated protein kinase 1)

DE (PAK1).
GN PAK2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96198078; PubMed=8626411;
RX Jakobi R., Chen C., Tuazon P.T., Traugh J.A.;
RT "Molecular cloning and sequencing of the cytosolic G protein-
activated protein kinase PAK 1.";
RL J. Biol. Chem. 271:6206-6211(1996).
CC -!- FUNCTION: The activated kinase acts on a variety of targets.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/P21 AND RAC1.
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STR20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
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CC -----
CC EMBL; U46915; AAC48537.1; -.
CC HSP; P24941; ICRP.
DR InterPro; IPR000095; PAKbox/RhoGndng.
DR InterPro; IPR000719; Prot Kinase.
DR InterPro; IPR008271; Ser Thr pkin AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 74 87 CRIB.
FT DOMAIN 88 248 LINKER.
FT DOMAIN 249 500 PROTEIN KINASE.
FT NP_BIND 255 263 ATP (BY SIMILARITY).
FT BINDING 278 278 ATP (BY SIMILARITY).
FT ACT_SITE 368 368 BY SIMILARITY.
SQ SEQUENCE 524 AA; 58027 MW; 397D1020EADFCA CRC64;
Query Match 29.1%; Score 900; DB 1; Length 524;
Best Local Similarity 34.4%; Pred. No. 4.6e-28;
Matches 207; Conservative 95; Mismatches 140; Indels 160; Gaps 12;
QY 4 KKKRVEISAPSNFHRVHTGFDQHEQKFTGLPROMQSLIE-----ESARRPKPLVDP 56
Db 67 KEKERPEISPPSDFEHTIHVGFDVAVTGFTGMPEQWARLLQTSNITKLEQKNPQAVLD- 125
QY 57 ACITSIQCAPKTIIVRGSKAGDKGALTLLDDFENMSVTRNSLRD--SPPPPARAQE 114
Db 126 -----VLKEYD-----SNTVKQKYLSTFP-----EK 147
QY 115 NGMPEEPATTARGGPKAGSRGAFHSEAGGSDRRRAGPEKPKSSREGSGGPQES 174
Db 148 DGFPSS-----GAPALNTKVSETSAVVTEEDD 173
QY 175 RDRKPLSGPDVGTQPAGLASGAKLAAGRPNTYPRADTHPSRGAQGEHDPVAPNGPS 234

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Db 174 DDEE-AAPPVIAPRPDHTKS-----IYTRVID-PIPAVGDSDH----- 210
QY 235 GGLAIPQSSSSSRPPTFRAGAPSPGVLGPHASEPOLAPPACTPAAPAVGPPGPRSPQR 234
Db 211 -----VDSGAKSSDK----- 222
QY 295 EPQVSHQEFRAALQVLVDPGDRSLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDL 354
Db 223 KTKMTDEEIMEXLRTIVSGDPKKYTRYEKLGQASGVFTATDVALGQFVAIQINL 282
QY 355 RKQORRELLFNEVIMRDYQHENVVEMYSYLVGDELVMVMEFLEGALTDIVTHRMNE 414
Db 283 QKQPKKELIINEILVMKELKNPKNVFNFLSYLVGDELVMVMEFLEGALTDIVTHRMNE 342
QY 415 EQIAAACLAVLQALSVLHAQVTHRDIKSDSILLTHDGRVKLSDFGFCQAVSKEVPRKS 474
Db 343 AQIAAACLAVLQALSVLHAQVTHRDIKSDSILLTHDGRVKLSDFGFCQAVSKEVPRKS 402
QY 475 LVGTPYMAPELISRLPYGPEVDIWSLGIWVIMVDEGPPYFNEPPLKAMKMDRLNLP 534
Db 403 MVGTPYMAPEVTRXAYGKVDIWSLGIWVIMVDEGPPYFNEPPLKAMKMDRLNLP 461
QY 535 LKMLHVKVSPKGLFDRLLVRDPAQRATAELLKHPFLAKAGPPASIVPL-----MRQ 587
Db 463 LQNPVKLSPIFRDLNCLMDVKEKRSKAKELLQHPFLKAKPLSLTPLIMAAKEAMKS 522
QY 588 NR 589
Db 523 NR 524

RESULT 9
PAK2 RAT
ID_PAK2_RAT STANDARD; PRT; 524 AA.
AC Q64303;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase PAK 2 (EC 2.7.1.-) (p21-activated
DE kinase 2) (PAK-2) (Gamma-PAK) (P62-PAK).
GN PAK2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.; AND PARTIAL SEQUENCE.
RC TISSUE=Brain, and Testis;
RX MEDLINE=96064759; PubMed=7592896;
RA Teo M., Manser E., Lim L.;
RT "Identification and molecular cloning of a p21cdc42/rac1-activated
RT serine/threonine kinase that is rapidly activated by thrombin in
RT platelets.";
RL J. Biol. Chem. 270:26690-26697(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Mabel T.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: The activated kinase acts on a variety of targets.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/P21 AND RAC1.
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S80221; AAB35608.1; -.
CC EMBL; U35345; AAA79064.1; -.
CC HSSP; P24941; 1CKP.
CC
CC InterPro; IPR000095; PAKbox/Rho-binding.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_Thr_pkin_AS.
CC InterPro; IPR002290; Ser_Thr_pkinase.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF00786; PBD; 1.
CC Pfam; PF00069; pkinase; 1.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00285; PBD; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS00108; CRIB; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC KW Transferase; Serine/threonine-protein kinase; ATP-binding;
CC Phosphorylation.
CC
CC FT DOMAIN 74 87 CRIB.
CC FT DOMAIN 88 248 LINKER.
CC FT DOMAIN 249 500 PROTEIN_KINASE.
CC FT NP_BIND 255 263 ATP (BY SIMILARITY).
CC FT BINDING 278 278 ATP (BY SIMILARITY).
CC FT ACT_SITE 368 368 BY SIMILARITY.
CC SQ SEQUENCE 524 AA; 57960 MW; A3F2FEB81C8D4294 CRC64;

Query Match 29.0%; Score 895; DB 1; Length 524;
Best Local Similarity 34.5%; Pred. No. 7.2e-28;
Matches 208; Conservative 92; Mismatches 141; Indels 162; Gaps 12;

QY 4 KRKKRVEISAPSNFHRVHTGFDQHEQKFTGLPROMQSLIE-----ESARPKPLVDP 56
Db 67 KEKERPEISPPSDFEHTIHVGFDAVTGETGPEQWARLLQTSNITKLOKKNQOAVLD- 125
QY 57 ACITSIQPGAKPTIVRGSKGAKDGALTLLDDEFNNMSVTRSNLSRRD--SPPPPAPARQE 114
Db 126 -----VLKFDV-----SNTVKQKYLSETPP-----EK 147
QY 115 NGMPE-EPATTARGGPGKAGSRGRFAGHSEAGGSGDRRAGPEKPKSRESGSGPQES 173
Db 148 DGFPSTGTPALNTKGS-----IYTRVID-----PIPA 205
QY 174 SRDKRPLSGFDVGTPOAGLASGAKLAGRPENTYPRADTDHPSRGAQGEHPDVAHPGS 233
Db 172 DDDDED-AAPPVIAPRPDHTKS-----IYTRVID-----PIPA 205
QY 234 AGGLAIPQSSSSSRPPTFRAGAPSPGVLGPHASEPOLAPPACTPAAPAVGPPGPRSPQ 293
Db 206 VGDSNVDSGAKSSDK-----Q 221
QY 294 REPQVSHQEFRAALQVLVDPGDRSLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMD 353
Db 222 KKKAKMTDEEIMEXLRTIVSGDPKKYTRYEKLGQASGVFTATDVALGQFVAIQIN 281
QY 354 LRQQRRELLFNEVIMRDYQHENVVEMYSYLVGDELVMVMEFLEGALTDIVTHRMN 413
Db 282 LQKQPKKELIINEILVMKELKNPKNVFNFLSYLVGDELVMVMEFLEGALTDIVTHRMN 341
QY 414 EQIAAACLAVLQALSVLHAQVTHRDIKSDSILLTHDGRVKLSDFGFCQAVSKEVPRRK 473
Db 342 EAQIAAACLAVLQALSVLHAQVTHRDIKSDSILLTHDGRVKLSDFGFCQAVSKEVPRRK 401
QY 474 SVGTPYMAPELISRLPYGPEVDIWSLGIWVIMVDEGPPYFNEPPLKAMKMDRLNLP 533
Db 402 TWGTPYMAPEVTRXAYGKVDIWSLGIWVIMVDEGPPYFNEPPLKAMKMDRLNLP 461
QY 534 LKMLHVKVSPKGLFDRLLVRDPAQRATAELLKHPFLAKAGPPASIVPL-----MR 586
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Db 462 ELONPEKLSPIFRDPLNRCLEMDVEKRSKAKELLQHPLFKLAKPLSLTLPLLAKEAMK 521

QY 587 QNR 589

Db 522 SNR 524

RESULT 10

PAK1 RAT STANDARD; PRT; 544 AA.

AC P35465; Q62934;

DT 01-JUN-1994 (Rel. 29, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-) (p21-activated kinase 1) (PAK-1) (P68-PAK) (Alpha-PAK) (Protein kinase MUK2).

GN PAK1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

[1]_TaxID=10116;

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=94150588; PubMed=8107774;

RA Manser E., Leung T., Salihuddin H., Zhao Z.-S., Lim L.;

RT "A brain serine/threonine protein kinase activated by Cdc42 and Rac1";

RL Nature 367:40-46(1994).

RN [2]

RP REVISIONS.

RA Zhao Z.-S.;

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Osada S.-I., Izawa M., Saito R., Mizuno K., Suzuki A., Hirai S.-I., Ohno S.;

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

RN [4]

RP TISSUE SPECIFICITY

RX MEDLINE=96027610; PubMed=7559638;

RA Manser E., Chong C., Zhao Z.-S., Leung T., Michael G., Hall C., Lim L.;

RT "Molecular cloning of a new member of the p21-Cdc42/Rac-activated kinase (PAK) family";

RL J. Biol. Chem. 270:25078(1995).

CC -!- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS. LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED GTPASES TO THE UNK MAP KINASE PATHWAY.

CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND CDC42/p21 AND RAC1 (BY SIMILARITY).

CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE BRAIN. WITH HIGHER EXPRESSION IN NEURONAL GROUPS ASSOCIATED WITH MOTOR FUNCTION, AND AT LOWER LEVELS IN THE SPLEEN.

CC -!- DEVELOPMENTAL STAGE: FOUND IN THE EMBRYONIC CNS WITH LITTLE EXPRESSION ELSEWHERE.

CC -!- PTM: Autophosphorylated when activated by CDC42/p21.

CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. ST202 subfamily.

CC -!- SIMILARITY: Contains 1 CRIB domain.

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CC EMBL; U23443; AAB95646.1; -

CC EMBL; U49953; AAB61533.1; -

DR PDB; 1EOA; 14-SEP-00.

DR InterPro; IPR000095; PAKbox/RhoBndng.

DR InterPro; IPR000719; Prot. kinase.

DR InterPro; IPR008271; Ser thr_pkin AS.

DR InterPro; IPR002290; Ser thr_pkinase.

DR InterPro; IPR001245; Tyr_pkinase.

DR Pfam; PF00786; PBD; 1.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Prot. kinase; 1.

DR SMART; SM00285; PBD; 1.

DR SMART; SM00220; S_TKc; 1.

DR PROSITE; PS00108; CRIB; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation; 3D-structure.

KW Phosphorylation; 3D-structure.

FT DOMAIN 75 88 CRIB

FT DOMAIN 89 268 LINKER.

FT DOMAIN 269 520 PROTEIN KINASE.

FT NP_BIND 275 283 ATP (BY SIMILARITY).

FT BINDING 298 298 ATP (BY SIMILARITY).

FT ACT_SITE 388 388 BY SIMILARITY.

SQ SEQUENCE 544 AA; 60577 MW; 93BE32D8222F5B7B CRC64;

Query Match 28.9%; Score 894; DB 1; Length 544;

Best Local Similarity 36.9%; Pred. No. 8.1e-28;

Matches 216; Conservative 82; Mismatches 165; Indels 122; Gaps 11;

QY 4 KKKKEVEISAPSNFHRVHTGFDQHEQKFTGLPROMQSLIESARRPKPLVDPACTISIQ 63

Db 68 KEKERPEISLPSDFEHTIHVGFDVATGFTGMPEQWARKLLQTSN----- 111

QY 64 PGAPKTIIVRGSKGAKDGALTLLIDFENMSVTRNSLRDSDPPPARAFQENGMEPEPAT 123

Db 112 -----ITKSEQKNPQAVLDVLEFFYNSKKT-SNSQYMS----- 144

QY 124 TARGFGKAGSRGRFAGHSEAGGSGDRRRAGPEKRPKSSREGSGQPQSSDKPLSGP 183

Db 145 -----FTDKSAEDYNSNTLNV-----KTVSETPAVPPVSEDE---DDD 180

QY 184 DVGTPQAGLASAKLAAGRPENT---YPRADTDHPSRGAQGEHDVAENGFSAGGLATP 240

Db 181 DDATPPP-----VIAPRPEHTKSVYTRSVI-----EPLPVTPT----- 213

QY 241 QSSSSSSRPPTRARGAPSPGVLGHASEPQLAPPACTPAAPAVPGPGSPRSPQREFQVS 300

Db 214 RDVAISPISTENNTTP-----PDALTTRNT-----EKQKKPKWS 248

QY 301 HEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIYCIATVRSRSGKLVAVKMDLRKQORR 360

Db 249 DEEILEKLSRISVSGDPKKKYTRFEKIGQASGTVYTAMDVATGQFVAIKOMNLOQPKK 308

QY 361 ELLFNEVIMRDYQHENVVVMYNSVLVGDVLMVMEFLGGALTDIVTHTRMNEEQIAAV 420

Db 309 ELIINELVIREKNKPNIVNYLDVSLVGDVLMVMEYLAGSLTDVVTETCDEGGIAAV 368

QY 421 CLAVLQALSVLHAQGVTHRDIKSDISILLTHDGRVKLSDFGCAQVSKEVPRRKSILVGTPY 480

Db 369 CRECLQALEFLHSNQVIHRDIKSDNILLGMDGSVKLTDFGCAQITPEQSKESTWVGTPY 428

QY 481 WNAPELISRLPYGPEVDVWLSGIMVIMWDGPPFPNEPPLKAMKMRNLNLPRLKNLHK 540

Db 429 WNAPEVTRKAYGPKVDIWSLGIMAEIMEIEGPPYINENPLRALYLIATNGTPELQNPKEK 488

QY 541 VSPSLKGFUDRLVLRDPAQRATAAELLKHPFLAKAGPPASIVPLM 585

Db 489 LSAIFRDLNRCLEMDVEKRSKAKELLQHPLFKLAKPLSLTLPL 533

RESULT 11

PAK1 HUMAN

ID_PAK1_HUMAN STANDARD; PRT; 545 AA.

AC Q13153; Q13567;

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Serine/threonine-protein kinase PAK 1 (EC 2.7.1.37) (p21-activated
 DE kinase 1) (PAK-1) (P65-PAK) (Alpha-PAK).
 GN PAK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97199447; PubMed=9395435;
 RA Sells M.A., Knaus U.G., Bagrodia S., Ambrose D.M., Bokoch G.M.,
 RA Chernoff J.;
 RT "Human p21-activated kinase (Pak1) regulates actin organization in
 RT mammalian cells.";
 RL Curr. Biol. 7:202-210 (1997).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=96398842; PubMed=8805275;
 RA Brown J.L., Stowers L., Baer M., Trejo J., Coughlin S., Chant J.;
 RT "Human Ste20 homologue hPAK1 links GTPases to the JNK MAP kinase
 RT pathway.";
 RL Curr. Biol. 6:598-605 (1996).
 RN [3]
 RN FUNCTION, AND INTERACTION WITH CDC2L1 AND CDC2L2.
 RX MEDLINE=22651041; PubMed=12624090;
 RA Chen S., Yin X., Zhu X., Yan J., Ji S., Chen C., Cai M., Zhang S.,
 RA Zong H., Hu Y., Yuan Z., Shen Z., Gu J.;
 RT "The C-terminal kinase domain of the p34cdc2-related PITSURE protein
 RT kinase (p110C) associates with p21-activated kinase 1 and inhibits
 RT its activity during anoikis";
 RL J. Biol. Chem. 278:20029-20036 (2003).
 CC -!- FUNCTION: The activated kinase acts on a variety of targets.
 CC Likely to be the GTPase effector that links the Rho-related
 CC GTPases to the JNK MAP kinase pathway. Activity inhibited in cells
 CC undergoing apoptosis, potentially due to binding of CDC2L1 and
 CC CDC2L2.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- COFACTOR: Magnesium.
 CC -!- SUBUNIT: Interacts tightly with GTP-bound but not GDP-bound
 CC CDC42/p21 and RAC1. Binds to the caspase-cleaved p110 isoform of
 CC CDC2L1 and CDC2L2, p110C, but not the full-length proteins.
 CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
 CC STE20 subfamily.
 CC -!- SIMILARITY: Contains 1 CRIB domain.
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 CC -----
 CC EMBL; U24152; AAC65441.1; --
 CC EMBL; U51120; AAC50590.1; --
 CC FIR; G01773; G01773.
 CC PDB; 1F3M; 29-NOV-00.
 CC Genew; HGNC:8590; PAK1.
 CC MIM; 602590; --
 CC GO; GO:0007254; P-JNK cascade; TAS.
 CC GO; GO:0006468; P-protein amino acid phosphorylation; TAS.
 CC InterPro; IPR000095; PAKBox/Rho-binding.
 CC InterPro; IPR000719; Prot kinase.
 CC InterPro; IPR008271; Ser Thr pkin AS.
 CC InterPro; IPR002290; Ser Thr pkinase.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC Pfam; PF00786; PBD; 1.
 CC Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS0108; CRIB; 1.
 DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW Apoptosis; Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW phosphorylation; 3D-structure.
 FT DOMAIN 75 88
 FT CRIB.
 FT DOMAIN 89 269
 FT LINKER.
 FT DOMAIN 270 521
 FT PROTEIN KINASE.
 FT NP_BIND 276 284
 FT ATP (BY SIMILARITY).
 FT BINDING 299 299
 FT ATP (BY SIMILARITY).
 FT ACT_SITE 389 389
 FT BY SIMILARITY.
 FT MUTAGEN 107 107
 FT L->F: CONSTITUTIVELY ACTIVE.
 FT CONFLICT 26 26
 FT V -> A (IN REF. 2).
 FT CONFLICT 237 237
 FT R -> L (IN REF. 2).
 FT CONFLICT 379 379
 FT F -> S (IN REF. 2).
 FT CONFLICT 503 503
 FT D -> E (IN REF. 2).
 SQ SEQUENCE 545 AA; 60661 MW; 14A1E70E6480CD7E CRC64;
 Query Match 28.9%; Score 892.5; DB 1; Length 545;
 Best Local Similarity 36.9%; Pred. No. 9.2e-28;
 Matches 216; Conservative 82; Mismatches 166; Indels 121; Gaps 11;
 QY 4 KRKRVEISAPSNFHRVITGDFDQHEQKFTGTPROMQSLIEESARRPKPLVDPACTISIQ 63
 DB 68 KEKERDEISLPSDFEHTIHVGFDVAVTGFTGMPEQWARLIQTSN----- 111
 QY 64 PGAPKTIVRGSGAKGKAGLTLTLLDFENMVSFTRNSLRDSDPPPARAQENGMPPEPAT 123
 DB 112 -----ITKSEQKNQPAVLVLEFYNSKKT-SNSQKYS----- 144
 QY 124 TARGPGKAGSRGFAGHSEAGSGDRRRAGGERKPKSRREGSGPQSSRRDPLSGP 183
 DB 145 -----FTDKSAEDVNSSNALNV-----KAVSETPAVPPVSEDED---DDD 181
 QY 184 DVGTPQAGLASAKLAAGRPNW---YPRADTHPSRGAQGEHPDVAENGPSAGGLAIP 240
 DB 182 DDATPPP-----VIAPRPEHTKSVYTRSVI-----EPLPVTPT----- 214
 QY 241 QSSSSSRPPTRARGAPSPGLGPHASEQLAPPACTPAAPVPGPPGPRSPQRPQVS 300
 DB 215 RDAVSPISPTENNITP-----PDALTRNT-----EKOKKKPKMS 249
 QY 301 HQQFRAALQVLVDGDPDRSYLDNFYKIGEGSTGIVCIATVRSGLVAVKMDLRKQRR 360
 DB 250 DBEILKLSIVSGDPKKKYTRFBKIGQSGSTVVTAMDVATGQEVAKQNNLQQPKK 309
 QY 361 ELLFNQVIMRDYQHENVVMNSYLVGLDELVWMEFEGGALTDIVTTRNNEEQIAAV 420
 DB 310 ELIINELVMRRNKNPNIVNYLDSYLVGLDELVWMEYLAGGSLTDVVTETCMDEGQIAAV 369
 QY 421 CLAVLQALSVLHAQGVHHRDIKSDSTLLTHDCRVKLSDFGCAOVSKVPRKSLVGTYP 480
 DB 370 CRECLQALEFLHSNQVHHRDIKSDNILLGMDGSKLTDGFCQAQITPPOSKKSTWGTYP 429
 QY 481 WMAPELISRLPYGPEVDIWSLGIWIMVDGPPPYFNEPPLKAMKIMRDNLPRLKLNHK 540
 DB 430 WMAPEVWTRKAYGPKVDIWSLGIWIMVEMEGEPPPYLNENPLRALVLIATNGTPELQNPCK 489
 QY 541 VPSLSKGFELDRLLVDRDPAQATAAELLKHPIFLAKAGPPASIVPLM 585
 DB 490 LSAIFRDFLNRLCLMDVKEKRSKELLQHQFLKIAKPLSLTFLI 534
 RESULT 12
 PAK1_MOUSE
 ID_FAK1_MOUSE STANDARD; PRT; 545 AA.
 AC O88643;
 DT 15-DEC-1998 (Rel. 37, Created)


```
CC CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC CC STE20 subfamily.
CC CC -!- SIMILARITY: Contains 1 CRIB domain.
CC CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC or send an email to license@isb-sib.ch)
CC CC -----
CC CC EMBL; M94719; AAA35111.1; -
CC CC EMBL; L04655; AAA35038.1; -
CC CC EMBL; L04655; AAA35039.1; -
CC CC EMBL; U11581; AAB69747.1; -
CC CC PIR; S28394; S28394.
CC CC HSP; O63450; 1A06.
CC CC Germline; 139274; -.
CC CC SGD; S0000999; STE20.
CC CC GO; GO:0000131; C:incipient bud site; IDA.
CC CC GO; GO:0005937; C:shmoo tip; IDA.
CC CC GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
CC CC GO; GO:000282; P:bud site selection; IMP.
CC CC GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
CC CC InterPro; IPR000095; PAKbox/RhoBndg.
CC CC InterPro; IPR000719; Prot_kinase.
CC CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC CC InterPro; IPR002290; Ser_thr_pkinase.
CC CC InterPro; IPR001245; Tyr_pkinase.
CC CC Pfam; PF00786; PBD; 1.
CC CC Pfam; PF00699; pkinase; 1.
CC CC PRINTS; PR00109; TYRKINASE.
CC CC ProDom; PD000001; Prot_kinase; 1.
CC CC SMART; SM00285; PBD; 1.
CC CC SMART; SM00220; S_TKc; 1.
CC CC PROSITE; PS0108; CRIB; 1.
CC CC PROSITE; PS0107; PROTEIN KINASE ATP; 1.
CC CC PROSITE; PS00011; PROTEIN KINASE DOM; 1.
CC CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
CC CC Pheromone response; Phosphorylation.
CC CC DOMAIN 337 350
CC CC CRIB.
CC CC FT DOMAIN 620 871
CC CC PROTEIN KINASE.
CC CC FT NP_BIND 626 634
CC CC ATP (BY SIMILARITY).
CC CC FT BINDING 649 649
CC CC ATP (BY SIMILARITY).
CC CC FT ACT_SITE 739 739
CC CC BY SIMILARITY.
CC CC FT CONFLICT 19 19
CC CC N -> S (IN REF. 2).
CC CC FT CONFLICT 134 134
CC CC I -> M (IN REF. 2).
CC CC FT CONFLICT 271 271
CC CC P -> S (IN REF. 2).
CC CC FT SEQUENCE 939 AA; 102362 MW; 69C1C12F5B87733C CRC64;
CC CC
CC CC Query Match 27.1%; Score 837; DB 1; Length 939;
CC CC Best Local Similarity 32.3%; Pred. No. 1.8e-25;
CC CC Matches 208; Conservative
CC CC
CC CC QY 9 VEISAFNFEHVHTGFDQHEQKFTGLPRQWQSLIESARRPKPLVDPACITSTQPCAPK 68
CC CC DB 335 LRISTPYNAKHIIHVGVDSVTGTYGLPEWEKLLTSSGI----- 374
CC CC
CC CC QY 69 TIVRGSKAGDGLTLLIDRFE-NMSVTRNSLRDSDPPPPARARQNGMPEEPATTARG 127
CC CC DB 375 -----SKREQQNQAVNDIVKFQDVTEING-----EDKMFKTNTTT-G 414
CC CC
CC CC QY 128 GPGKAGSRGRFAGHSEAGGGGDRRRRAGPEKPKSRREGSGGPPESDRDKPLS----- 181
CC CC DB 415 LPGS-----PQVST-----PPANSFNKPPSTSDSHN 441
CC CC
CC CC QY 182 -GPDVGTVPQAGLASGAKLAAGRPENTVPADTDPGRGAQGEHDVAPNGSPSAGGLAIP 240
CC CC DB 442 YGSRGTGTPMSNHWS-----PTLNTDSSANGKFIISRPAKPPSSASAP 488
CC CC
CC CC QY 241 -----QSSSSSSRPPTTRAGAPSPGVLGPHAS-----BPQLAPP----- 274
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Db 489 IIKSPVWNSAANVSPLKQTHAPTTPNRTSPNRSSISRNATLKKEQPLPPIPTPKSKTSP 548
QY 275 -----ACTPAAPAVPGPPRSPQEPORVSHE-----QFRAALQ 309
Db 549 IISTAHTPQQAQPKAPAQTVTTPTSKPAQASLSKELNEKKREERRKKQLYAKLN 608
QY 310 LVVDPGDPSPRSLDNFKIKIGEGSTGIVCIATVRSSGKLVAVKMDLURKQORRELLNEVVI 369
Db 609 EICSDGDPSTKYANLVKIQGASGGVYAYEIGTGVSVVAIKQMNLEKQPKKELIINEILV 668
QY 370 MRDYQHEVNVEMNSYLVGDELWVMEFEGGALTDIVHTFMNEEQIAAACLAVLQALS 429
Db 669 MKGSXHPNIVNPFIDSYVLKGLWVIMEYMEGSLTDVVVTHCILTEGQIGAVCRETLISGLE 728
QY 430 VLHAQGVTHRDIKSDSIILLTHDGRVKLSDFGCAQVSKVEPRPKSLVGTGPPYMWAPELISR 489
Db 729 FLHSGKVLHRDIKSDNILLSMEGDIKLTDFGCAQINELNLEKTTVMGTGTPYMWAVEVSR 788
QY 490 LPYGEVDIWSLGINVIMVGDGEPYFNEPPIKAMKMRDNPRIKLNHUKVSPSLKGL 549
Db 789 KEYGPKVDIWSLGINMIEMIEGEPYLNETPLRALYLIATNGTTPKLKEPENLSSSLKKFL 848
QY 550 DRLIVRDPAAQATAAELLKHPFLAK-AGPPASIVPLMRQNRTR 591
Db 849 DWCLCVPEDRASATELLHDEYITETAANSSSLAPLVKLARLK 891
RESULT 15
PAK1_SCHPO STANDARD; PRT; 658 AA.
ID PAK1_SCHPO
AC P50527;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase pak1/shk1 (EC 2.7.1.-).
OS PAK1 OR SHK1 OR ORB2 OR SPBCL604.14C.
OC Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=96112805; PubMed=8846783;
RX Otilie S., Miller P.J., Johnson D.I., Creasy C.L., Sells M.A.,
RA Bagrodia S., Forsburg S.L., Chernoff J.,
RT "Fission yeast pak1+ encodes a protein kinase that interacts with
RL Cdc42p and is involved in the control of cell polarity and mating.";
RN EMBO J. 14:5908-5919(1995).
[2]
SEQUENCE FROM N.A.
RP Marcus S.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Scouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Cellins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds R., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkkaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
```

RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RA "The genome sequence of *Schizosaccharomyces pombe*.";
RL Nature 415:871-880(2002).
RN [4].
RP SEQUENCE OF 119-658 FROM N.A.
RX MEDLINE=95320235; PubMed=7597098;
RA Marcus S., Polverino A., Chang E., Robbins D., Cobb M.H.,
RA Wiegler M.;
RT "Shk1, a homolog of the *Saccharomyces cerevisiae* Ste20 and mammalian
RT p38PAK protein kinases, is a component of a Ras/cdc42 signaling
RT module in the fission yeast *Schizosaccharomyces pombe*.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:6180-6184(1995).
CC -I- FUNCTION: Acts in signal transduction. Involved in the control of
CC cell polarity and mating.
CC -I- SUBUNIT: Forms an activated complex with GTP-bound ras-like cdc42.
CC Interacts with shk1 via its amino-terminal regulatory domain.
CC Shk1, cdc42 and pak1/shk1 are able to form a ternary complex in
CC vivo. May interact with byr2.
CC -I- PTM: Autophosphorylated on serine residues.
CC -I- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -I- SIMILARITY: Contains 1 CRIB domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; U22371; AAC49125.1; -;
DR ENBL; AL034433; CRA22347.1; -;
DR ENBL; L41552; XAB52609.1; -;
DR FIR; S60170; S60170.
DR FIR; T39500; T39500.
DR HSSP; Q00534; 1B18.
DR GeneDB SPombe; SPBC1604.14c; -;
DR InterPro; IPR000095; PAKBox/RhoBndg.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 147 160 CRIB.
FT DOMAIN 85 88 POLY-SER.
FT DOMAIN 234 237 POLY-SER.
FT DOMAIN 246 249 POLY-SER.
FT DOMAIN 263 267 POLY-SER.
FT DOMAIN 386 637 PROTEIN_KINASE.
FT NP_BIND 392 400 ATP (BY SIMILARITY).
FT BINDING 415 415 ATP (BY SIMILARITY).
FT ACT_SITE 505 505 BY SIMILARITY.
FT CONFLICT 492 495 GLOH -> LYSD (IN REF. 1).

FT CONFLICT 537 537 R -> P (IN REF. 1).
SQ SEQUENCE 658 AA; 72358 MW; 69D72E5C925021E5 CRC64;
Query Match 26.7%; Score 823.5; DB 1; Length 658;
Best Local Similarity 31.5%; Pred. No. 4.4e-25;
Matches 188; Conservative 113; Mismatches 193; Indels 103; Gaps 12;
QY 6 KKRVEISAPSNFHRVHTGDDQHEQKETGLPRQWQSLE-----ESARRPKPLVDPA 58
Db 142 RKSTVSSPDPKHVTHVGFNYDTGFTGMTQALLKVSIGITKSEGVQHPQAVLDAMA 201
QY 59 ITSQPGAPKTIVRGSKGAKDGALTLLEDFFENMVTRSNLRDSDPPPARARQENMP 118
Db 202 FYS-----QSKYLEGA-----KPPFFPRETEK----- 225
QY 119 EEPATTARGPGKAGSRGRFAGHSEAGGSGRRRAGPEKRPKSSREGSGGPQESSRDKR 178
Db 226 -----PLLSVSALSSSSSHLQPTSATSSSSRLYP-----SR 255
QY 179 PLSGPDVGTTPQAGLASGAKLAAGRPNTYPRADTHPSRGAOGEPHD--VAPNGPSAGG 236
Db 256 P-----APTTPASSSSSSPLSSQTVKTTTNSARQPSPLVSSKSTDNIIRSHSPV--- 305
QY 237 LAIPQSSSSSRPPTTRARGAPSPGVLPGLPHASEP--OLAPPACTPAAPAVP---GPGPR 290
Db 306 LLTPQTLSSTETKHIR-----PNNSTYQRRAEISTPKKAVATPKVEAFSAPR 354
QY 291 SPOREPQSVSHEQ- FRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIAIVRSSGKLAV 349
Db 355 LQKRAPRQSQNSAVLAKLQSI CNPKNPTLLYRNFVKIGQSGDVYSARQVGNLSVAI 414
QY 350 KMDLRKQORRELLFNEVIMRDYOHENVMYNSYLVDGLVMVEFLEGGALTDIVTH 409
Db 415 KXNINQPKPKKEPIVNEILVMKSHHKNI VNFDTTFYKSELMMVMYEMRGSSITEVVTN 474
QY 410 TRMNEQIAAVCLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKEV 469
Db 475 NTLSEGGIAAICKETLEGLQHLHENGIVHRDIKSDNILLSLQGDIKLDTDFGCAQIDSNM 534
QY 470 PRKSLVGTPTVMWAPELISRLPYGPEVDIWSLGIWVIMVYDGEPPYFNEPPLKAMKIRD 529
Db 535 TKRTTMVGTPTVMWAPVWTRKEYGFKVDVWSLGIWVIMVYDGEPPYFNEPPLKALVLIAT 594
QY 530 NLPPRLKNLHKVSPSLKGLDRLLVDPDPAORATAAELLKHPFLAKAGPPASIVPLMR 586
Db 595 IGTPTKISRPELLSSVFHDFLSKSLTYNPKQRPSSGELLRHPLKQAVPVVSSLIPLIK 651

Search completed: September 29, 2004, 18:02:01

Job time : 21.5132 secs

Blank

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 17:57:52 ; Search time 6.54412 Seconds
(without alignments)
1308.205 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452

Sequence: 1 KQORRELFNEVIMRDYRH.....LQALAVLHAQGVTHSDIKTD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	303	67.0	540	2 T19956	hypothetical prote
2	303	67.0	542	2 T19952	hypothetical prote
3	277	61.3	544	2 S40482	serine/threonine-s
4	277	61.3	545	2 G01773	p21-activated prot
5	276	61.1	544	2 A57597	beta-p21-activated
6	269	59.5	544	2 I49376	p21 activated kina
7	266	58.8	622	2 T15467	hypothetical prote
8	265.5	58.7	525	2 S58682	protein kinase, p2
9	256	56.6	1230	2 T18256	probable serine/th
10	256	56.6	1230	2 T18259	serine/threonine p
11	255	56.4	939	2 S28394	probable serine/th
12	235.5	52.1	378	2 T26684	hypothetical prote
13	231.5	51.2	842	2 S60402	protein kinase CLA
14	231	51.1	658	2 T39500	serine/threonine-s
15	227	50.2	658	2 S60170	protein kinase Pak
16	220.5	48.8	589	2 T38086	serine/threonine-p
17	203.5	45.0	655	2 S51884	probable protein k
18	177.5	39.3	819	2 A53714	protein kinase (EC
19	167.5	37.1	829	2 T29372	hypothetical prote
20	154	34.1	1102	2 JC6316	probable protein k
21	153	33.8	836	2 B98716	probable serine/th
22	151.5	33.5	1401	2 T39225	MAP kinase kinase
23	148.5	33.1	545	2 T33748	hypothetical prote
24	148.5	32.9	652	2 T39722	serine/threonine p
25	146.5	32.4	1192	2 T18611	probable serine/th
26	146.5	32.4	1246	2 G89287	protein H39E22.1 [
27	146	32.3	1233	2 T30989	serine/threonine p
28	145.5	32.2	1075	2 T27623	hypothetical prote
29	145.5	32.2	1080	2 T27622	hypothetical prote

30	145.5	32.2	1314	2 S19488	probable membrane
31	145	32.1	471	2 T39232	probable serine th
32	144.5	32.0	348	2 T37521	Ca2+/calmodulin-de
33	143	31.6	653	2 T34356	hypothetical prote
34	142.5	31.5	690	2 C96572	protein F12M16.4 [
35	141.5	31.3	1051	1 JW0051	serine/threonine-s
36	141.5	31.3	1579	2 S59801	protein kinase SSK
37	138.5	30.6	312	2 T38525	serine/threonine p
38	137.5	30.4	1062	2 S46367	protein kinase CDC
39	136	30.1	415	2 JQ2251	calcium/calmodulin
40	135.5	30.0	460	2 S58882	protein kinase Cds
41	135.5	30.0	883	2 A96662	hypothetical prote
42	135	29.9	1206	2 T34021	protein kinase SK2
43	135	29.9	1231	2 T18532	serine/threonine pr
44	135	29.9	1233	2 T14157	serine/threonine p
45	133	29.4	1097	2 F96538	hypothetical prote

ALIGNMENTS

RESULT 1

T19956

hypothetical protein C45B11.1b - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000

C:Accession: T19956

R:McMurray, A.

submitted to the EMBL Data Library, June 1996

A:Reference number: Z19202

A:Accession: T19956

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-540 <WIL>

A:Cross-references: EMBL:Z74029; PIDN:CAA98433.1; GSPDB:GN00023; CESP:C45B11.1b

A:Experimental source: clone C45B11

C:Genetics:

A:Gene: CESP:C45B11.1b

A:Map position: 5

A:Introns: 13/2; 62/3; 104/2; 231/3; 367/2; 468/3

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 67.0%; Score 303; DB 2; Length 540;

Best Local Similarity 67.4%; Pred. No. 2.1e-20;

Matches 60; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYRHENVMYNSLYGDELWVYMEFEGGALTDIVTHRMNEE 60

Db 284 KQORRELFNEVSIILRQYQHPNIVRFFSSHLDVDELWVYMEFEGGSLDIVTATMTPEP 343

QY 61 QIANVCLAVLQALAVLHAQGVTHSDIKTD 89

Db 344 QIATISRQVLGALDFUARKVTHRIKSD 372

RESULT 2

T19952

hypothetical protein C45B11.1a - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000

C:Accession: T19952

R:McMurray, A.

submitted to the EMBL Data Library, June 1996

A:Reference number: Z19202

A:Accession: T19952

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-542 <WIL>

A:Cross-references: EMBL:Z74029; PIDN:CAA98429.1; GSPDB:GN00023; CESP:C45B11.1a

A:Experimental source: clone C45B11

C:Genetics:

A:Gene: CESP:C45B11.1a

A:Map position: 5

A; Introns: 13/2; 62/3; 104/2; 233/3; 369/2; 470/3
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology

Query Match 67.0%; Score 303; DB 2; Length 542;
Best Local Similarity 67.4%; Pred. No. 2.1e-20;
Matches 60; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYLVDGLWVMEFEGGALTDIVTHTRMNEE 60
DB 286 KQORRELLFNEVIMRDYRHENVMYNSYLVDGLWVMEFEGGALTDIVTHTRMNEE 60

QY 61 QIAAVCLAVLQALAVLHAQGVVHSIDIKTD 89
DB 346 QIATISRQVIGALDFLHARKVIRHDIKSD 374

RESULT 3
S40482
serine/threonine-specific protein kinase (EC 2.7.1.1) - rat
C; Species: Rattus norvegicus (Norway rat)
C; Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C; Accession: S40482
R; Manser, E.; Leung, T.; Salihuddin, H.; Zhao, Z.; Lim, L.
Nature 367, 40-46, 1994
A; Title: A brain serine/threonine protein kinase activated by Cdc42 and Rac1.
A; Reference number: S40482; MUID:94150588; PMID:8107774
A; Accession: S40482
A; Molecule type: mRNA
A; Residues: 1-544 <MAN>
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
C; Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F; 267-520/Domain: protein kinase homology <KIN>
F; 275-283/Region: protein kinase ATP-binding motif

Query Match 61.3%; Score 277; DB 2; Length 544;
Best Local Similarity 58.4%; Pred. No. 5e-18;
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYLVDGLWVMEFEGGALTDIVTHTRMNEE 60
DB 304 QQPKKELIINEILVMRENKPNINVLDSYLVGDELWVMEYLAGGSLTDVVTCTMDRG 363

QY 61 QIAAVCLAVLQALAVLHAQGVVHSIDIKTD 89
DB 364 QIAAVCRECLQALEFLHSNQVIRHDIKSD 392

RESULT 4
G01773
p21-activated protein kinase - human
C; Species: Homo sapiens (man)
C; Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999
C; Accession: G01773
R; Chernoff, J.
submitted to the EMBL Data Library, April 1995
A; Reference number: G08374
A; Accession: G01773
A; Status: preliminary; translated from GB/EMBL/DBUJ
A; Molecule type: mRNA
A; Residues: 1-545 <CHE>
A; Cross-references: EMBL:U24152; NID:g780805; PIDN:AAA65441.1; PID:g780806
C; Geneticks:
A; Gene: Pak1
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
F; 268-521/Domain: protein kinase homology <KIN>

Query Match 61.3%; Score 277; DB 2; Length 545;
Best Local Similarity 58.4%; Pred. No. 5.1e-18;
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYLVDGLWVMEFEGGALTDIVTHTRMNEE 60
DB 305 QQPKKELIINEILVMRENKPNINVLDSYLVGDELWVMEYLAGGSLTDVVTCTMDRG 364

QY 61 QIAAVCLAVLQALAVLHAQGVVHSIDIKTD 89
DB 365 QIAAVCRECLQALEFLHSNQVIRHDIKSD 393

RESULT 5
A57597
beta-p21-activated protein kinase - rat
N; Alternate names: beta-PAK
C; Species: Rattus norvegicus (Norway rat)
C; Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 24-Sep-1999
C; Accession: A57597
R; Manser, E.; Chong, C.; Zhao, Z.S.; Leung, T.; Michael, G.; Hall, C.; Lim, L.
J. Biol. Chem. 270, 25070-25078, 1995
A; Title: Molecular cloning of a new member of the p21-Cdc42/Rac-activated kinase (PAK) family.
A; Reference number: A57597; MUID:96027610; PMID:7559638
A; Accession: A57597
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-544 <MAN>
A; Cross-references: GB:U33314; NID:g1039424; PIDN:AAC52268.1; PID:g1039425
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
C; Keywords: ATP
F; 266-519/Domain: protein kinase homology <KIN>
F; 274-282/Region: protein kinase ATP-binding motif

Query Match 61.1%; Score 276; DB 2; Length 544;
Best Local Similarity 58.4%; Pred. No. 6.2e-18;
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYLVDGLWVMEFEGGALTDIVTHTRMNEE 60
DB 303 QQPKKELIINEILVMRENKPNINVLDSYLVGDELWVMEYLAGGSLTDVVTCTMDRG 362

QY 61 QIAAVCLAVLQALAVLHAQGVVHSIDIKTD 89
DB 363 QIAAVCRECLQALDFLHSNQVIRHDIKSD 391

RESULT 6
I49376
P21 activated kinase-3 - mouse
C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C; Accession: I49376
R; Bagrodia, S.; Taylor, S.J.; Creasy, C.L.; Chernoff, J.; Cerione, R.A.
J. Biol. Chem. 270, 22731-22737, 1995
A; Title: Identification of a mouse P21Cdc42/Rac activated kinase.
A; Reference number: I49376; MUID:96032693; PMID:7559398
A; Accession: I49376
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: mRNA
A; Residues: 1-544 <RES>
A; Cross-references: EMBL:U39738; NID:g1079713; PIDN:AAC52354.1; PID:g1079714
C; Geneticks:
A; Gene: mPAK-3
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
C; Keywords: ATP
F; 266-519/Domain: protein kinase homology <KIN>
F; 274-282/Region: protein kinase ATP-binding motif

Query Match 59.5%; Score 269; DB 2; Length 544;
Best Local Similarity 57.3%; Pred. No. 2.7e-17;
Matches 51; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYLVDGLWVMEFEGGALTDIVTHTRMNEE 60
DB 303 QQPKKELIINEILVMRENKPNINVLDSYLVGDELWVMEYLAGGSLTDVVTCTMDRG 362

QY 61 QIAAVCLAVLQALAVLHAQGVVHSIDIKTD 89
DB 363 QIAAVCRECLQALDFLHSNQVIRHDIKSD 391

RESULT 7
T15467
hypothetical protein C09B8.7 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 19-May-2000
C:Accession: T15467
R:Stelljes, L.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of *C. elegans* cosmid C09B8.
A:Reference number: S61138
A:Accession: T15467
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-622 <STE>
A:Cross-references: EMBL:U29612; NID:9868273; PID:9868279; PIDN:AAA68805.1; CESP:C09B8.7
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:C09B8.7
A:Introns: 107/1, 142/3, 192/1, 260/3; 291/3; 481/1; 505/3; 546/3; 570/3
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
Query Match 58.8%; Score 266; DB 2; Length 622;
Best Local Similarity 56.8%; Pred. No. 6e-17;
Matches 50; Conservative 18; Mismatches 20; Indels 0; Gaps 0;
QY 2 QORRELLFNEVIMRDYRHENVVEMNSYLVDGLVWVMEFLGGGALTDIVTHTRMNEEQ 61
DB 381 QPKKELIINEILVMKGNPNIVNFDLSYLVCDGLVWVMEYLAGGSLTDVVVTACMDE 440
QY 62 IAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 441 IAAVCEVLQALEFLHSRHHVHDIKSD 468
RESULT 8
S58682
protein kinase, p21-activated (EC 2.7.1.1) - human
N:Alternate names: protein kinase PAK65; S6/H4 kinase
C:Species: *Homo sapiens* (man)
C>Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 24-Sep-1999
C:Accession: S58682; S55258; S55304; S58690; A57441
R:Sells, M.; Knause, U.J.; Bagrodia, S.; Ambrose, D.; Bokoch, G.M.; Chernoff, J.
submitted to the EMBL Data Library, April 1995
A:Description: Human p21-activated protein kinases regulate actin organization in mammal
A:Reference number: S58682
A:Accession: S58682
A:Molecule type: DNA
A:Residues: 1-525 <SEL>
A:Cross-references: EMBL:U24153; NID:g780807; PIDN:AAA65442.1; PID:g780808
R:Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.
EMBO J. 14, 1970-1978, 1995
A:Title: A novel serine kinase activated by rac1/CDC42Hs-dependent autophosphorylation i
A:Reference number: S55258; MUID:95262637; PMID:7744004
A:Accession: S55258
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 'MESTQKSNLEL', 31-89, 'T', 91-149, 'F', 151-224, 'T', 226-328, 'R', 330-338, 340-525
A:Accession: S55304
A:Molecule type: protein
A:Residues: 402-418 <MAW>
R:Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.
EMBO J. 14, 4385, 1995
A:Reference number: S58690; MUID:96016211; PMID:7556080
A:Contents: erratum
A:Accession: S58690
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-30 <MAF>
R:Benner, G.E.; Dennis, P.B.; Masaracchia, R.A.
J. Biol. Chem. 270, 2121-21128, 1995
A:Title: Activation of an S6/H4 kinase (PAK 65) from human placenta by intramolecular an

A:Reference number: A57441; MUID:95403344; PMID:7673144
A:Accession: A57441
A:Molecule type: protein
A:Residues: 197-216; 402, 'S', 404-409 <BEN>
A:Experimental source: placenta
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonin
F:247-501/Domain: protein kinase homolog <KIN>
F:255-263/Region: protein kinase ATP-binding motif
F:197,402/Binding site: phosphate (Ser) (covalent) #status predicted
Query Match 58.7%; Score 265.5; DB 2; Length 525;
Best Local Similarity 57.8%; Pred. No. 5.5e-17;
Matches 52; Conservative 18; Mismatches 19; Indels 1; Gaps 1;
QY 1 KQORRELLFNEVIMRDYRHENVVEMNSYLVDGLVWVMEFLGGGALTDIVTHTRMNE 59
DB 284 KQPKKELIINEILVMKGNPNIVNFDLSYLVCDGLVWVMEYLAGGSLTDVVVTACMDE 343
QY 60 EQIAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 344 AQIAVCRECLQALEFLHANQVHDIKSD 373
RESULT 9
T18256
probable serine/threonine-specific protein kinase (EC 2.7.1.1) - yeast (*Candida albicans*)
C:Species: *Candida albicans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T18256
R:Leberer, E.; Marcus, D.; Broadbent, I.D.; Clark, K.L.; Dignard, D.; Ziegelbauer, K.; Sc
proc. Natl. Acad. Sci. U.S.A. 93, 13217-13222, 1996
A:Title: Signal transduction through homologs of the Ste20p and Ste7p protein kinases car
A:Reference number: Z18843; MUID:97075145; PMID:8917571
A:Accession: T18256
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1230 <LEB>
A:Cross-references: EMBL:L47210; NID:g2276410; PID:g2286042; PIDN:AAB5439.1
C:Keywords: phosphotransferase; serine/threonine-specific protein kinase
Query Match 56.6%; Score 256; DB 2; Length 1230;
Best Local Similarity 50.6%; Pred. No. 1e-15;
Matches 45; Conservative 21; Mismatches 23; Indels 0; Gaps 0;
QY 1 KQORRELLFNEVIMRDYRHENVVEMNSYLVDGLVWVMEFLGGGALTDIVTHTRMNEE 60
DB 989 QQPKKELIINEILVMKGNPNIVNFDLSYLVCDGLVWVMEYLAGGSLTDIVTHSYMTEG 1048
QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 1049 QIGVVCRETGLKGLKFLHSGVHDIKSD 1077
RESULT 10
T18259
serine/threonine protein kinase homolog - yeast (*Candida albicans*)
C:Species: *Candida albicans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-May-2000
C:Accession: T18259
R:Kohler, J.R.; Fink, G.R.
Proc. Natl. Acad. Sci. U.S.A. 93, 13223-13228, 1996
A:Title: *Candida albicans* strains heterozygous and homozygous for mutations in mitogen-ac
A:Reference number: Z11118; MUID:97075146; PMID:8917572
A:Accession: T18259
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1230 <KOH>
A:Cross-references: EMBL:U73457; NID:g1657953; PID:g1737181; PIDN:AAB38875.1
C:Genetics:
A:Note: CST20
Query Match 56.6%; Score 256; DB 2; Length 1230;

A;Cross-references: SGD:S0005242; MIPS:YNL298w
A;Map position: 14L
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; pleckstrin repeat homology
C;Keywords: ATP; phosphotransferase
F;544-825/Domain: protein kinase homology <KIN>

Query Match 51.1%; Score 231.5; DB 2; Length 842;
Best Local Similarity 40.4%; Pred. No. 1e-13;
Matches 36; Conservative 28; Mismatches 25; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYL-VGDELWVWMEFLEGGALTDIV----- 52
Db 600 KQPKKEFIVNEILVMKSHHKNVFNFDITFFYKSELMMVMYMRGGSLETVVNTNLTSEG 659

QY 53 -TTRMNEEQIAAACLAVLQALAVLHAQGVTHSDIKTD 89
Db 660 NSHSPLEPQIAYIVRTCCQGLKFLHDKHIIHRDIKSD 697

RESULT 14

T39500

serine/threonine-specific protein kinase (EC 2.7.1.1-) paki-shk1 - fission yeast (Schizosaccharomyces pombe)

N;Alternate names: Ste20 homologous protein kinase 1

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000

C;Accession: T39500; T45523

R;Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, December 1998

A;Reference number: Z21859

A;Accession: T39500

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-658 <BEC>

A;Cross-references: EMBL:AL034433; PIDN:CAA22347.1; GSPDB:GNO00666; SPDB:SPBC1604.14C

A;Experimental source: strain 972h-; cosmid C1604

R;Marcus, S.

submitted to the EMBL Data Library, April 1997

A;Reference number: Z22999

A;Accession: T45523

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-658 <MAR>

A;Cross-references: EMBL:L41552; PIDN:AAB52609.1

C;Genetics:

A;Gene: shk1; SPBC1604.14C

A;Map position: 1

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
C;Keywords: hydrolase; phosphotransferase; signal transduction

Query Match 51.1%; Score 231; DB 2; Length 658;
Best Local Similarity 40.4%; Pred. No. 1e-13;
Matches 36; Conservative 28; Mismatches 25; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYL-VGDELWVWMEFLEGGALTDIVTHTRMNEE 60
Db 421 QQPKKEFIVNEILVMKSHHKNVFNFDITFFYKSELMMVMYMRGGSLETVVNTNLTSEG 480

QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
Db 481 QIAAICKETLEGLHENGIVHRDIKSD 509

RESULT 15

S60170

protein kinase Pak1 - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 24-Sep-1999

C;Accession: S60170

R;Ottillie, S.; Miller, P.J.; Johnson, D.I.; Creasy, C.L.; Sells, M.A.; Bagrodia, S.; For

EMBO J. 14, 5908-5919, 1995

A;Title: Fission yeast paki(+) encodes a protein kinase that interacts with Cdc42p and

A;Reference number: S60170; MUID:96112805; PMID:8846783

A;Accession: S60170

A;Status: preliminary
A;Molecule type: mRNA

A;Residues: 1-658 <OTT>

A;Cross-references: EMBL:U22371; NID:g1122910; PIDN:AAC49125.1; PID:g1122911

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology

C;Keywords: ATP

F;384-637/Domain: protein kinase ATP-binding motif

F;392-400/Region: protein kinase ATP-binding motif

Query Match 50.2%; Score 227; DB 2; Length 658;
Best Local Similarity 39.3%; Pred. No. 2.4e-13;
Matches 35; Conservative 29; Mismatches 25; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYL-VGDELWVWMEFLEGGALTDIVTHTRMNEE 60
Db 421 QQPKKEFIVNEILVMKSHHKNVFNFDITFFYKSELMMVMYMRGGSLETVVNTNLTSEG 480

QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
Db 481 QIAAICKETLEGLHENGIVHRDIKSD 509

Search completed: September 29, 2004, 18:05:38
Job time : 7.54412 secs

Blank

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 17:41:57 ; Search time 20.1559 Seconds
(without alignments)
1393.197 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452

Sequence: 1 KQORRELFNEVIMRDYRH.....LQALAVLHAQGVIIHSIDIKTD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rviro:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	443	98.0	407	11 Q8KOU2	Q8KOU2 mus musculus
2	443	98.0	593	11 Q8BTW9	Q8btw9 mus musculus
3	443	98.0	593	11 Q8OZ97	Q8oz97 mus musculus
4	436	96.5	240	4 Q8NCH5	Q8nch5 homo sapien
5	436	96.5	467	4 Q8ULS8	Q8uls8 homo sapien
6	436	96.5	483	4 Q8NDE3	Q8nde3 homo sapien
7	436	96.5	501	4 Q8N4E1	Q8n4e1 homo sapien
8	421	93.1	650	13 Q90W62	Q90w62 xenopus lae
9	409	90.5	229	11 Q9CS71	Q9cs71 mus musculus
10	407	90.0	719	11 Q8C015	Q8c015 mus musculus
11	402	88.9	719	11 Q8TB93	Q8tb93 homo sapien
12	399	88.3	719	11 Q8BVB0	Q8bvbo mus musculus
13	366	81.0	639	5 Q9VXE5	Q9vxe5 drosophila
14	366	81.0	639	5 Q960J8	Q960j8 drosophila
15	366	81.0	639	5 Q96372	Q96372 drosophila
16	303	67.0	540	5 Q9U3M1	Q9u3m1 caenorhabdi

17	303	67.0	542	5 Q18637	Q18637 caenorhabdi
18	283	62.6	704	5 Q9V113	Q9v113 drosophila
19	283	62.6	704	5 Q24190	Q24190 drosophila
20	279	61.7	704	5 Q24213	Q24213 drosophila
21	277	61.3	447	4 Q86W79	Q86w79 homo sapien
22	277	61.3	553	4 Q75561	Q75561 homo sapien
23	277	61.3	577	13 Q803Z0	Q803z0 brachydanio
24	276	61.1	410	4 Q8WVK5	Q8wvk5 homo sapien
25	276	61.1	544	4 Q9P0J8	Q9p0j8 homo sapien
26	276	61.1	544	11 Q8K1R6	Q8kir6 mus musculus
27	276	61.1	559	6 Q7Z3Z8	Q7z3z8 homo sapien
28	276	61.1	559	6 Q7YQL4	Q7yql4 pan troglod
29	276	61.1	559	6 Q7YQL3	Q7yql3 pongo pygma
30	276	61.1	559	11 Q8K1R5	Q8kir5 mus musculus
31	276	61.1	584	13 Q8AXB4	Q8axb4 xenopus lae
32	274	60.6	524	11 Q9QYU0	Q9qyu0 rattus norv
33	274	60.6	524	11 Q8CIN4	Q8cin4 mus musculus
34	273	60.4	525	13 Q57318	Q57318 xenopus lae
35	273	60.4	527	13 Q9PW62	Q9pw62 xenopus lae
36	272	60.2	540	4 Q9Y6B5	Q9y6b5 homo sapien
37	270	59.7	517	13 Q8AW67	Q8aw67 brachydanio
38	266	58.8	300	5 Q86GT9	Q86gt9 caenorhabdi
39	266	58.8	523	5 Q86GU0	Q86gu0 caenorhabdi
40	266	58.8	569	5 Q22041	Q22041 caenorhabdi
41	266	58.8	572	5 Q94133	Q94133 caenorhabdi
42	266	58.8	572	5 Q17850	Q17850 caenorhabdi
43	262	58.0	914	3 Q7Z8E9	Q7z8e9 magnaportha
44	261	57.7	517	13 Q919C2	Q919c2 xenopus lae
45	257.5	57.0	644	3 Q9HEW5	Q9hew5 cryptococcu

ALIGNMENTS

RESULT 1

Q8KOU2 PRELIMINARY; PRT; 407 AA.

AC Q8KOU2; DT 01-OCT-2002 (Tremblrel. 22, Created)

DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Hypothetical protein (Fragment).

GN PAK4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1] SEQUENCE FROM N.A.

RP Strausberg R;

RC TISSUE=Retina;

RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

RL EMBL; BC030389; AAH30389.1; -.

DR MGD; MGI:1917834; Pak4.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR000719; Prot kinase.

DR InterPro; IPR002290; Ser Thr kinase.

DR Pfam; PF00069; pkinase; 1.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00220; S_TKc; 1.

DR SMART; SM00219; TyrKc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.

DR Hypothetical protein; ATP-binding; Transferase.

FT NON_TER 1

SQ SEQUENCE 407 AA; 44339 MW; 921689734DF9D710 CRC64;

Query Match 98.0%; Score 443; DB 11; Length 407;

Best Local Similarity 97.8%; Pred. No. 1.2e-43;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYRHENVMYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 60
|||||
Db 172 KQORRELFNEVIMRDYRHENVMYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 231

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
|||||
Db 232 QIAAVCLAVLQALAVLHAQGVHSDIKTD 260

RESULT 2

Q8BTW9 PRELIMINARY; PRT; 593 AA.
AC Q8BTW9
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Serine/threonine-protein kinase PAK 4 (Similar to
DE P21(CDKN1A)-activated kinase 4).
GN PAK4 OR 5730488L07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [2]
SEQUENCE FROM N.A.
RP STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK088512; BAC40396.1; -;
DR EMBL; BC048238; AAF48238.1; -;
DR MGD; MGI:1917834; Pak4.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKBox/RhoBndng.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR ProDom; PD000069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Kinase.

Query Match 98.0%; Score 443; DB 11; Length 593;
Best Local Similarity 97.8%; Pred. No. 1.8e-43;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYRHENVMYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 60
|||||
Db 358 KQORRELFNEVIMRDYRHENVMYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 417

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
|||||

Db 418 QIAAVCLAVLQALAVLHAQGVHSDIKSD 446

RESULT 3

Q80Z97 PRELIMINARY; PRT; 593 AA.
AC Q80Z97;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE P21-activated protein kinase 4.
DE Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=BALB/c;
RX MEDLINE=22526742; PubMed=12529371;
RA Lu Y., Pan Z.Z., Devaux Y., Ray P.;
RT "P21-activated Protein Kinase 4 (PAK4) Interacts with the Keratinocyte
RT Growth Factor Receptor and Participates in Keratinocyte Growth Factor-
RT mediated Inhibition of Oxidant-induced Cell Death.";
RL J. Biol. Chem. 278:10374-10380(2003).
DR EMBL; AY217016; AAO61496.1; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKBox/RhoBndng.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Ser_thr_kinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Kinase.

Query Match 98.0%; Score 443; DB 11; Length 593;
Best Local Similarity 97.8%; Pred. No. 1.8e-43;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYRHENVMYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 60
|||||
Db 358 KQORRELFNEVIMRDYRHENVMYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 417

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
|||||

RESULT 4

Q8NCH5 PRELIMINARY; PRT; 240 AA.
AC Q8NCH5;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Hypothetical protein FLJ90247.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,

Query Match 98.0%; Score 443; DB 11; Length 593;
Best Local Similarity 97.8%; Pred. No. 1.8e-43;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYRHENVMYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 60
|||||
Db 358 KQORRELFNEVIMRDYRHENVMYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 417

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
|||||

RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
 RA Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
 RT "NEDO human cDNA sequencing project";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK074728; F:ATP binding; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00219; TyRK; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 KW Hypothetical protein; ATP-binding; Transferase.
 SQ SEQUENCE 240 AA; 27332 MW; E3C686288D4913B6 CRC64;

Query Match 96.5%; Score 436; DB 4; Length 240;
 Best Local Similarity 95.5%; Pred. No. 4.1e-43;
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 60
 DB 5 KQORRELLFNEVIMRDYRHENNVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 64

QY 61 QIAAVCLAVLQALVLAHQGVHSDIKTD 89
 DB 65 QIAAVCLAVLQALVLAHQGVHSDIKTD 93

RESULT 5

Q9ULS8
 ID Q9ULS8 PRELIMINARY; PRT; 467 AA.
 AC Q9ULS8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein KIAA1142 (Fragment).
 GN KIAA1142.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20039618; PubMed=10574461;
 RA Hirose M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
 RT "Characterization of cDNA clones selected by the GeneMark analysis
 from size-fractionated cDNA libraries from human brain.";
 RL DNA Res. 6:329-336(1999).
 DR EMBL; AB032968; BAA86456.1; -.
 DR HSSP; Q63450; 1A06.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000095; PAKbox/RhoGAP.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS50108; CRIB; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 KW Hypothetical protein; ATP-binding; Transferase.
 FT NON_TER 1
 SQ SEQUENCE 467 AA; 51464 MW; EC342B8F5C5E3940 CRC64;

Query Match 96.5%; Score 436; DB 4; Length 467;
 Best Local Similarity 95.5%; Pred. No. 9.2e-43;
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 60
 DB 232 KQORRELLFNEVIMRDYRHENNVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 231

QY 61 QIAAVCLAVLQALVLAHQGVHSDIKTD 89
 DB 292 QIAAVCLAVLQALVLAHQGVHSDIKTD 320

RESULT 6

O8NDE3
 ID O8NDE3 PRELIMINARY; PRT; 483 AA.
 AC O8NDE3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN DKFZF547G182.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Wiemann S.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL834236; CAD38914.1; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000095; PAKbox/RhoGAP.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00219; TyRK; 1.
 DR PROSITE; PS50108; CRIB; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 KW Hypothetical protein; ATP-binding; Transferase.
 FT NON_TER 1
 SQ SEQUENCE 483 AA; 52787 MW; 8976E3BF0B8818B6 CRC64;

Query Match 96.5%; Score 436; DB 4; Length 483;
 Best Local Similarity 95.5%; Pred. No. 9.6e-43;
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 60
 DB 248 KQORRELLFNEVIMRDYRHENNVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 307

QY 61 QIAAVCLAVLQALVLAHQGVHSDIKTD 89
 DB 308 QIAAVCLAVLQALVLAHQGVHSDIKTD 336

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RESULT 7
Q8N4E1 PRELIMINARY; PRT; 501 AA.
AC Q8N4E1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to RIKEN cDNA 5730488L07 gene.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034511; AAH34511.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/RhoGndng.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 501 AA; 54940 MW; 6E86240CEB5E79D CRC64;

Query Match 96.5%; Score 436; DB 4; Length 501;
Best Local Similarity 95.5%; Pred. No. 1e-42; Mismatches 3; Indels 0; Gaps 0;
Matches 85; Conservative 3;

QY 1 KQORRELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMELEGALTDIVTHRMNEE 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
266 KQORRELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMELEGALTDIVTHRMNEE 325

QY 61 QIAAVCLAVLQALVLAHQGVTHSDIKTD 89
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
326 QIAAVCLAVLQALVLAHQGVTHSDIKTD 354

RESULT 8
Q90W62 PRELIMINARY; PRT; 650 AA.
AC Q90W62;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PAKS protein.
GN PAKS.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RA Cau J., Faure S., Delsert C., Morin N.;
RT "A novel xenopus p21 activated kinase expressed in brain.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277826; CAC40979.1; -.

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DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/RhoGndng.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 650 AA; 73736 MW; 9274DC6CADC4A081 CRC64;

Query Match 93.1%; Score 421; DB 13; Length 650;
Best Local Similarity 89.9%; Pred. No. 8e-41; Mismatches 7; Indels 0; Gaps 0;
Matches 80; Conservative 7;

QY 1 KQORRELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMELEGALTDIVTHRMNEE 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
415 KQORRELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMELEGALTDIVTHRMNEE 474

QY 61 QIAAVCLAVLQALVLAHQGVTHSDIKTD 89
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
475 QIAAVCLAVLQALVLAHQGVTHSDIKTD 503

RESULT 9
Q9CS71 PRELIMINARY; PRT; 229 AA.
AC Q9CS71;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 5730488L07Rik protein (Fragment).
GN PAK4 OR 5730488L07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085860; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK017713; BAB30889.1; -.
DR HSSP; Q63450; 1A06.
DR MGD; MGI:1917834; Pak4.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.

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DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR000719; Prot kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot kinase; 1.
 DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
 KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
 FT NON_TER 1 1
 SQ SEQUENCE 229 AA; 25896 MW; D9CF2CA73CED941E CRC64;

Query Match 90.5%; Score 409; DB 11; Length 229;
 Best Local Similarity 97.6%; Pred. No. 5.9e-40;
 Matches 80; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 8 LFNEVIMRDYRHENVMYNSYLVDGLWVMEFLEGGALTDIVTHTRMNEEQIAAVCL 67
 Db 1 LFNEVIMRDYRHENVMYNSYLVDGLWVMEFLEGGALTDIVTHTRMNEEQIAAVCL 60
 QY 68 AVLQALAVLHAQGVHSDIKTD 89
 Db 61 AVLQALAVLHAQGVHSDIKSD 82

RESULT 10
 Q8C015 PRELIMINARY; PRT; 719 AA.
 AC Q8C015; 21, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Serine/threonine-protein kinase PAK 5.
 GN 2900083L08RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 DR EMBL; AK032593; BAC27939.1; -;
 DR MGD; MGI:1920334; 2900083L08RIK.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR000095; PAKbox/Rho-binding.
 DR InterPro: IPR000719; Prot kinase.
 DR InterPro: IPR002290; Ser thr pkinase.
 DR Pfam: PF00786; PBD; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S.TKC; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00108; CRIB; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 SQ SEQUENCE 719 AA; 80948 MW; 5E16D2318C238C8D CRC64;

Query Match 90.0%; Score 407; DB 11; Length 719;
 Best Local Similarity 87.8%; Pred. No. 4e-39;
 Matches 78; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYRHENVMYNSYLVDGLWVMEFLEGGALTDIVTHTRMNEE 60
 Db 484 KQORRELFNEVIMRDYRHENVMYNSYLVDGLWVMEFLEGGALTDIVTHTRMNEE 543
 QY 61 QTAANCLAVLQALVHAQGVHSDIKTD 89
 Db 544 QIATVCLSVLRALSVLHNOGVHSDIKSD 572

RESULT 11
 Q8TB93 PRELIMINARY; PRT; 719 AA.
 AC Q8TB93; 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE P21(CDKN1A)-activated kinase 7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC024179; AAH24179.1; -;
 DR HSSP; P24941; 1BUH.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR000095; PAKbox/Rho-binding.
 DR InterPro: IPR000719; Prot kinase.
 DR InterPro: IPR002290; Ser thr pkinase.
 DR Pfam: PF00786; PBD; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S.TKC; 1.
 DR PROSITE; PS00108; CRIB; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 719 AA; 80794 MW; 536CB5DE65DA9FC3 CRC64;

Query Match 88.9%; Score 402; DB 4; Length 719;
 Best Local Similarity 86.5%; Pred. No. 1.6e-38;
 Matches 77; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 QY 1 KQORRELFNEVIMRDYRHENVMYNSYLVDGLWVMEFLEGGALTDIVTHTRMNEE 60
 Db 484 KQORRELFNEVIMRDYRHENVMYSSYLVDGLWVMEFLEGGALTDIVTHTRMNEE 543
 QY 61 QTAANCLAVLQALVHAQGVHSDIKTD 89
 Db 544 QIATVCLSVLRALSVLHNOGVHSDIKSD 572

RESULT 12
 Q8VB0 PRELIMINARY; PRT; 719 AA.
 AC Q8VB0; 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Serine/threonine-protein kinase PAK 5.
 GN 2900083L08RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
DR EMBL; AK079080; BAC37528.1; --
DR MGD; MGI:1920334; 2900083L08Rik.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/RhoGndng.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR0109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyRKc; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
SQ SEQUENCE 719 AA; 80967 MW; F1E33DCB8C39875B CRC64;
Query Match 88.3%; Score 399; DB 11; Length 719;
Best Local Similarity 86.5%; Pred. No. 3.5e-38;
Matches 77; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY 1 KQORELLFNEVIMRDYRHENVVMYNSYLVGDELWVMELEGALTDIVTHRMNEE 60
Db 484 KQORELLFNEVIMRDYRHENVVMYNSYLVGDELWVMELEGALTDIVTHRMNEE 543
QY 61 QIAAVCLAVLQMLAVHQAQGVTHSDIKTD 89
Db 544 QIATVCLSLKALSYLHNGQVTHRIKSD 572
RESULT 13
QVXES
ID Q9VXE5 PRELIMINARY; PRT; 639 AA.
AC Q9VXE5; Q9TYH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG18532 protein (p21 activated kinase related protein).
GN MBT OR CG18582.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flossler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Houslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., McLeod M.P., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celnik S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galie R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jatali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnik S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Seale S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=99035549; PubMed=9811608;
RA Melzig J., Rein K.H., Schaefer U., Pfister H., Jaeckle H.,
RA Heisenberg M., Raabe T.;
RT "A protein related to p21-activated kinase (PAK) that is involved in
RT neurogenesis in the Drosophila adult central nervous system";
RL Curr. Biol. 8:1223-1226 (1998).

```
DR EMBL; AB003502; AAF48629.2; -.
DR EMBL; AJ011578; CAA09699.1; -.
DR FlyBase; FBgn0025743; mbt.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/Rhobndg.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 639 AA; 69620 MW; 414D217F0AEBC1C6 CRC64;

Query Match 81.0%; Score 366; DB 5; Length 639;
Best Local Similarity 78.7%; Pred. No. 2.4e-34;
Matches 70; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 KQORRELFNEVVIMRDYRHENVVMYNSYLVGDELWVWMEFLGGALTDIVTHTRMNEE 60
DB 403 KQORRELFNEVVIMRDYRHENVVMYNSYLVGDELWVWMEFLGGALTDIVTHSRMDEE 462
QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 463 QIATVCKQCLKALAYLHSGQVHRDIKSD 491

RESULT 15
Q960J8 PRELIMINARY; PRT; 639 AA.
AC Q960J8;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE LD47563P.
GN MBT OR CG18582.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]_TaxID=7227;
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunco J., Pacleb J., Pargass V., Park S., Phouanavong S., Man K.,
RA Yu C., Lewis S.E., Rubin G.M., Celnik S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RE EMBL; AY052023; AAK93447.1; -.
DR HSSP; P24941; 1BUH.
DR FlyBase; FBgn0025743; mbt.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/Rhobndg.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
```

```
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 639 AA; 69592 MW; 2145317F0AE8F554 CRC64;

Query Match 81.0%; Score 366; DB 5; Length 639;
Best Local Similarity 78.7%; Pred. No. 2.4e-34;
Matches 70; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 KQORRELFNEVVIMRDYRHENVVMYNSYLVGDELWVWMEFLGGALTDIVTHTRMNEE 60
DB 403 KQORRELFNEVVIMRDYRHENVVMYNSYLVGDELWVWMEFLGGALTDIVTHSRMDEE 462
QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 463 QIATVCKQCLKALAYLHSGQVHRDIKSD 491

RESULT 15
Q96372 PRELIMINARY; PRT; 639 AA.
AC Q96372;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE STE20 serine/threonine protein kinase homolog.
GN MBT OR CG18582.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]_TaxID=7227;
RP SEQUENCE FROM N.A.
RA Melnick M.B.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RE EMBL; AF031517; AAD01935.1; -.
DR HSSP; P24941; 1BUH.
DR FlyBase; FBgn0025743; mbt.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/Rhobndg.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 639 AA; 69653 MW; 414D2177224C43C6 CRC64;

Query Match 81.0%; Score 366; DB 5; Length 639;
Best Local Similarity 78.7%; Pred. No. 2.4e-34;
Matches 70; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 KQORRELFNEVVIMRDYRHENVVMYNSYLVGDELWVWMEFLGGALTDIVTHTRMNEE 60
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Db 403 KQORELLFNEVWINRDYHHPNIVETYSFLVNDELWVMEYLEGGALTDIVTHSRMDEE 462
QY 61 QIAAYCLAVLQALAVLHAGQVHSDIKTD 89
Db 463 QIATVCKOCLKALAYLHSGQVHHRDIKSD 491

Search completed: September 29, 2004, 18:04:41
Job time : 20.1559 secs

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OM protein - protein search, using sw model

Run on: September 29, 2004, 17:36:56 ; Search time 23.2971 Seconds
(without alignments)
1079.395 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452

Sequence: 1 KQORRELFNEVIMRDYRH.....LQALAVLHAQGVHSGDIKTD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*

- 1: Genesecp1980s:*
- 2: Genesecp1990s:*
- 3: Genesecp2000s:*
- 4: Genesecp2001s:*
- 5: Genesecp2002s:*
- 6: Genesecp2003as:*
- 7: Genesecp2003bs:*
- 8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	452	100.0	89	3 AAY59139	Aay59139 Mouse ser
2	436	96.5	240	4 AAM93297	Aam93297 Human pol
3	436	96.5	240	7 ADC37303	Adc37303 Nuclear f
4	436	96.5	250	3 AAY59129	Aay59129 Human PAK
5	436	96.5	293	7 ADEL5851	Adel5851 PAK4KD pr
6	436	96.5	398	2 AAY55941	Aay55941 Human PAK
7	436	96.5	438	7 ADC37305	Adc37305 Nuclear f
8	436	96.5	501	7 ADC37309	Adc37309 Nuclear f
9	436	96.5	591	2 AAY55964	Aay55964 Full leng
10	436	96.5	591	3 AAY59128	Aay59128 Human ser
11	436	96.5	591	7 ADC37307	Adc37307 Nuclear f
12	436	96.5	591	7 ADD89973	Add89973 Human can
13	436	96.5	620	4 ABG19308	Abg19308 Novel hum
14	407	90.0	547	4 AAG67825	Aag67825 Human pol
15	407	90.0	719	4 AAM38963	Aam38963 Human pol
16	402	88.9	632	4 AAB85788	Aab85788 Human kin
17	402	88.9	719	4 AAB85705	Aab85705 Novel pro
18	402	88.9	719	4 AAE02187	Aae02187 Human p21
19	402	88.9	719	7 ADC37451	Adc37451 Nuclear f
20	379	83.8	311	4 AAB20336	Aab20336 Human PAK
21	379	83.8	641	5 AAE16269	Aae16269 Human kin
22	379	83.8	681	2 AAY55940	Aay55940 Human PAK
23	379	83.8	681	3 AAB03967	Aab03967 Signal tr
24	379	83.8	681	3 AAB03970	Aab03970 Mutant si
25	379	83.8	681	3 AAB03971	Aab03971 Mutant si

ALIGNMENTS

RESULT 1

AAY59139
ID AAY59139 standard; protein; 89 AA.

XX
AC AAY59139;

XX
08-MAR-2000 (first entry)

XX
Mouse serine/threonine kinase, PAK4 partial protein sequence.

XX
PAK4; serine/threonine kinase; GTPase; intracellular signal cascade; Rac;
KW Cdc42H; morphogenesis; mitogenesis; JNK; p38 MAP kinase; mouse;
KW actin polymerization; filopodia; cancer; arthritis.

XX
Mus sp.

XX
W09963073-A1.

XX
09-DEC-1999.

XX
21-MAY-1999; 99WO-US011341.

XX
21-MAY-1998; 98US-00082737.

XX
(UYCO) UNIV COLUMBIA NEW YORK.

XX
Minden A;

XX
WPI; 2000-072881/06.

XX
N-PSDB; AAZ40658.

XX
Novel mammalian nucleic acid useful for treating cancer and arthritis.

XX
Disclosure; Page 44; 95pp; English.

XX
The invention relates to an isolated mammalian nucleic acid that encodes
CC PAK4, a novel serine/threonine kinase or its mutant homolog. PAK4 is an
CC effector for the GTPases Rac and Cdc42Hs which are involved in
CC intracellular signal cascades, morphogenesis and mitogenesis, and
CC activate the JNK and p38 MAP kinase pathways. Inhibiting interaction of
CC PAK4 with these enzymes will thus result in inhibition of actin
CC polymerization and formation of filopodia. The PAK4 nucleic acid used for
CC recombinant production of the protein, and as a source of probes for
CC identifying homologous sequences and of (anti)sense oligonucleotides for
CC inhibiting PAK4 expression. The protein, or its fragments, are used to
CC raise specific antibodies and these are useful as ligands for therapeutic
CC inhibition of interaction between PAK4 and its native binding partners.
CC Inhibition of PAK4 activity or expression is used for treatment of cancer

Aab20337 Human PAK
Abp64709 Human pro
Abu11508 Human MDD
Aag63230 Amino aci
Abb60665 Drosophil
Abb66726 Drosophil
Abb64989 Drosophil
Aar50951 Receptor
Aay84633 Amino aci
Aaw15266 Beta-amy1
Ade62673 Rat Prote
Ada05670 Human NOV
Abu07464 Protein d
Abg30251 Novel hum
Aay84634 Amino aci
Aaw72757 Human dou
Aae14906 Human P21
Aay55958 Human STE
Aay84632 Amino aci
Aaw15265 Rat beta-

26 379 83.8 681 4 AAB20337
27 379 83.8 681 5 ABP64709
28 379 83.8 701 6 ABU11508
29 376 83.2 681 4 AAG63230
30 366 81.0 575 4 ABB60665
31 283 62.6 704 4 ABB66726
32 283 62.6 704 4 ABB64989
33 278 61.5 465 2 AAR50951
34 277 61.3 244 3 AAY84633
35 277 61.3 465 2 AAW15266
36 277 61.3 544 7 ADE62673
37 277 61.3 545 6 ADA05670
38 277 61.3 545 6 ABU07464
39 277 61.3 587 4 ABG30251
40 276 61.1 245 3 AAY84634
41 276 61.1 544 2 AAW72757
42 276 61.1 544 6 AAE14906
43 276 61.1 545 2 AAY55958
44 274 60.6 244 3 AAY84632
45 274 60.6 520 2 AAW15265

CC and arthritis. The present sequence represents the partial sequence of
 CC mouse PAK4
 XX
 SQ Sequence 89 AA;

Query Match 100.0%; Score 452; DB 3; Length 89;
 Best Local Similarity 100.0%; Pred. No. 1e-50;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60
 DB 1 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60

QY 61 QIAAVCLAVLQALAVLHAQGVHSIDKTD 89
 DB 61 QIAAVCLAVLQALAVLHAQGVHSIDKTD 89

RESULT 2
 ID AAM93297 standard; protein; 240 AA.
 XX
 AC AAM93297;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide, SEQ ID NO: 2793.
 XX
 KW Human; full length cDNA; cDNA synthesis; oligo-capping.
 XX
 OS Homo sapiens.
 XX
 PN EP1130094-A2.
 XX
 PD 05-SEP-2001.
 XX
 PF 07-JUL-2000; 2000EP-00114089.
 XX
 PR 08-JUL-1999; 99JP-00194486.
 XX
 PR 11-JAN-2000; 2000JP-00118774.
 XX
 PR 02-MAY-2000; 2000JP-00183765.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 DR WPI; 2001-524255/58.
 XX
 DR N-PSDB; AAK94217.
 XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 XX
 PS Claim 8; SEQ ID NO 2793; 1380pp + Sequence Listing; English.
 XX
 CC The invention relates to primers for synthesising full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesising the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in CD-ROM
 CC format directly from EPO

XX SQ Sequence 240 AA;
 Query Match 96.5%; Score 436; DB 4; Length 240;
 Best Local Similarity 95.5%; Pred. No. 5e-48;
 Matches 85; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60
 DB 5 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 64

QY 61 QIAAVCLAVLQALAVLHAQGVHSIDKTD 89
 DB 65 QIAAVCLAVLQALAVLHAQGVHSIDKTD 93

RESULT 3
 ID ADC37303 standard; protein; 240 AA.
 XX
 AC ADC37303;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 136.
 XX
 KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
 KW cancer; infectious disease; bone disease; AIDS;
 KW neurodegenerative disease; ischaemic disorder; Antiinflammatory;
 KW immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
 KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003048202-A2.
 XX
 PD 12-JUN-2003.
 XX
 PF 03-DEC-2002; 2002WO-JP012644.
 XX
 PR 03-DEC-2001; 2001JP-00368692.
 XX
 PR 05-DEC-2001; 2001US-0335829P.
 XX
 PR 03-OCT-2002; 2002JP-00291302.
 XX
 PR 04-OCT-2002; 2002US-0415769P.
 XX
 PA (ASAH) ASahi KASEI KK.
 XX
 PI Matsuda A, Muramatsu S;
 XX
 DR WPI; 2003-505282/47.
 XX
 DR N-PSDB; ADC37302.
 XX
 PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
 PT useful for treating inflammation, autoimmune diseases, cancers,
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
 PT ischemic disorders.
 XX
 PS Claim 1; SEQ ID NO 136; 938pp; English.
 XX
 CC The present invention relates to novel proteins and their coding
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
 CC kappaB). The proteins and their coding sequences are useful for treating
 CC a disease associated with NF-kappaB activation, such as inflammation,
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
 CC neurodegenerative diseases, or ischaemic disorders.
 XX
 SQ Sequence 240 AA;
 Query Match 96.5%; Score 436; DB 7; Length 240;
 Best Local Similarity 95.5%; Pred. No. 5e-48;
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60
 DB 5 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 64

QY 61 QIAAVCLAVLQALAVLHAQGVHSIDKTD 89
 DB 65 QIAAVCLAVLQALAVLHAQGVHSIDKTD 93

```

RESULT 4
AAY59129
ID AAY59129 standard; protein; 250 AA.
XX
AC AAY59129;
XX
DT 08-MAR-2000 (first entry)
XX
DE Human PAK4 kinase domain fragment.
XX
KW PAK4; serine/threonine kinase; GTPase; intracellular signal cascade; Rac;
KW Cdc42H; morphogenesis; mitogenesis; JNK; p38 MAP kinase; human;
KW actin polymerization; filopodia; cancer; arthritis; kinase domain.
XX
OS Homo sapiens.
XX
PN WO963073-A1.
XX
PD 09-DEC-1999.
XX
PF 21-MAY-1999; 99WO-US011341.
XX
PR 21-MAY-1998; 98US-00082737.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Minden A;
XX
DR WPI; 2000-072881/06.
XX
PT Novel mammalian nucleic acid useful for treating cancer and arthritis.
XX
PS Disclosure; Fig 1C; 95pp; English.
XX
CC The invention relates to an isolated mammalian nucleic acid that encodes
CC PAK4, a novel serine/threonine kinase or its mutant homolog. PAK4 is an
CC effector for the GTPases Rac and Cdc42Hs which are involved in
CC intracellular signal cascades, morphogenesis and mitogenesis, and
CC activate the JNK and p38 MAP kinase pathways. Inhibiting interaction of
CC PAK4 with these enzymes will thus result in inhibition of actin
CC polymerization and formation of filopodia. The PAK4 nucleic acid used for
CC recombinant production of the protein, and as a source of probes for
CC identifying homologous sequences and of (anti)sense oligonucleotides for
CC inhibiting PAK4 expression. The protein, or its fragments, are used to
CC raise specific antibodies and these are useful as ligands for therapeutic
CC inhibition of interaction between PAK4 and its native binding partners.
CC Inhibition of PAK4 activity or expression is used for treatment of cancer
CC and arthritis. The present sequence represents the kinase domain fragment
CC of human serine/threonine kinase, PAK4
XX
SQ Sequence 250 AA;
Query Match 96.5%; Score 436; DB 3; Length 250;
Best Local Similarity 95.5%; Pred. No. 5.3e-48;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 KQORRELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVVHTRMNEE 60
Db 33 KQORRELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVVHTRMNEE 92
QY 61 QTAAVCLAVLQALAVLHAQGVHSDIKTD 89
Db 93 QTAAVCLAVLQALSVLHAQGVHSDIKTD 121
RESULT 5
ADE15851
ID ADE15851 standard; protein; 293 AA.
XX
AC ADE15851;
XX

```

```

DT 29-JAN-2004 (first entry)
XX
DE PAK4KD protein.
XX
KW PAK4KD protein.
XX
OS Homo sapiens.
XX
PN WO2003087816-A1.
XX
PD 23-OCT-2003.
XX
PF 08-APR-2003; 2003WO-US010878.
XX
PR 09-APR-2002; 2002US-0371018P.
PR 02-DEC-2002; 2002US-0430567P.
XX
PA (STRU-) STRUCTURAL GENOMIX INC.
XX
PI Antonyseamy SS, Feil I, Buchanan SG, Post KW, Liu Y, Lorber D;
XX
DR WPI; 2003-853974/79.
XX
PT Producing a computer-readable database comprising the three-dimensional
PT molecular structural coordinates of a binding pocket of a PAK4KD protein,
PT comprises introducing the structural coordinates into a computer.
XX
PS Claim 17; SEQ ID NO 5; 421pp; English.
XX
CC The present invention relates to producing a computer-readable database
CC comprising the three-dimensional molecular structural coordinates of a
CC binding pocket of a PAK4KD protein, comprising introducing the structural
CC coordinates to into a computer to produce a database containing the
CC molecular structural coordinates of the protein or binding pocket. The
CC method is useful for producing a machine-readable database for
CC identifying and designing inhibitors, activators and mutants of PAK4KD,
CC PAK4KD crystals and compounds or compositions that affect PAK4KD
CC activity. The present sequence represents a primer of the invention.
XX
SQ Sequence 293 AA;
Query Match 96.5%; Score 436; DB 7; Length 293;
Best Local Similarity 95.5%; Pred. No. 6.6e-48;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 KQORRELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVVHTRMNEE 60
Db 58 KQORRELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVVHTRMNEE 117
QY 61 QTAAVCLAVLQALAVLHAQGVHSDIKTD 89
Db 118 QTAAVCLAVLQALSVLHAQGVHSDIKTD 146
RESULT 6
AAY55941
ID AAY55941 standard; protein; 398 AA.
XX
AC AAY55941;
XX
DT 18-FEB-2000 (first entry)
XX
DE Human PAK5 protein.
XX
KW Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;
KW antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;
KW neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;
KW vulnery; STE20; protein kinase; STIK2; STIK3; STIK4; STIK5; STIK6; STIK7;
KW ZC1; ZC2; ZC3; ZC4; KHS2; SUL01; SUL03; GEK2; PAK4; PAK5; antagonist;
KW antibody; gene therapy; rheumatoid arthritis; arteriosclerosis; asthma;
KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KW rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
KW myocardial infarction; cardiovascular disease; stroke; renal failure;

```

KW oxidative stress-related neurodegenerative disorder; Parkinson's disease;
 KW amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
 KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
 KW mesangial disorder; growth regulation; wound healing; T cell activation;
 KW immunosuppressant.

XX
 OS Homo sapiens.
 XX
 XX
 PN WO9953036-A2.
 XX
 PD 21-OCT-1999.
 XX
 PF 13-APR-1999; 99WO-US008150.
 XX
 PR 14-APR-1999; 98US-0081784F.
 XX
 PA (SUGEN-) SUGEN INC.
 XX
 XX Plowman G, Martinez R, Whyte D;
 PI WPI; 1999-611301/52.
 DR N-PSDB; AA240493.
 XX

PT Novel kinase-related polypeptides used for the diagnosis and treatment of
 PT Kinase-related diseases and disorders.

XX
 PS Disclosure; Page 310-312; 387pp; English.
 XX
 CC This sequence represents a novel STE20-related protein kinase. The
 CC invention relates to nucleic acid molecule encoding a kinase polypeptide
 CC selected from STUK2, STUK3, STUK4, STUK5, STUK6, STUK7, ZC1, ZC2, ZC3,
 CC ZC4, KHS2, SUJ1, SUJ3, GEK2, PAK4 and PAK5. The proteins are used to
 CC identify agonists and antagonists, and to raise antibodies. The
 CC polynucleotides are useful in gene therapy protocols. The polynucleotides,
 CC polypeptides, antibodies, antagonists and agonists may be used to treat
 CC diseases such as immune-related disorders and diseases (e.g. rheumatoid
 CC arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g.
 CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
 CC rhinitis, autoimmunity, and organ transplantation, chronic inflammation,
 CC pelvic disease, multiple sclerosis, organ transplantation, myocardial
 CC infarction, cardiovascular disease, stroke, renal failure, oxidative
 CC stress-related neurodegenerative disorders (e.g. amyotrophic lateral
 CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,
 CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
 CC mellitus, fibrotic and mesangial disorders. The proteins may also be
 CC useful for cell growth regulation (e.g. in wound healing), T cell
 CC activation, mitosis control, and as immunosuppressants

XX
 SQ Sequence 398 AA;
 Query Match 96.5%; Score 436; DB 2; Length 398;
 Best Local Similarity 95.5%; Pred. No. 1e-47;
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVMYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60
 DB 163 KQORRELLFNEVIMRDYRHENVVMYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 222

QY 61 QIAAVCLAVLQALVLAHQGVTHSDIKTD 89
 DB 223 QIAAVCLAVLQALVLAHQGVTHSDIKTD 251

RESULT 7
 ADC37305
 ID ADC37305 standard; protein; 438 AA.

XX
 AC ADC37305;
 XX
 XX 18-DEC-2003 (first entry)
 XX
 XX Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 138.

KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
 KW cancer; infectious disease; bone disease; AIDS;
 KW neurodegenerative disease; ischaemic disorder; Antiinflammatory;
 KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
 KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human.

XX
 OS Homo sapiens.
 XX
 XX
 PN WO2003048202-A2.
 XX
 PD 12-JUN-2003.
 XX
 PF 03-DEC-2002; 2002WO-JP012644.
 XX
 PR 03-DEC-2001; 2001JP-00368692.
 XX
 PR 05-DEC-2001; 2001US-0335829P.
 PR 03-OCT-2002; 2002JP-00291302.
 PR 04-OCT-2002; 2002US-0415769P.
 XX
 XX (ASAH) ASAH KASEI KK.
 PA
 XX Matsuda A, Muramatsu S;
 XX
 XX WPI; 2003-505282/47.
 DR N-PSDB; ADC37304.
 XX

PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
 PT useful for treating inflammation, autoimmune diseases, cancers,
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
 PT ischemic disorders.

PS Claim 1; SEQ ID NO 138; 938pp; English.
 XX
 CC The present invention relates to novel proteins and their coding
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
 CC kappaB). The proteins and their coding sequences are useful for treating
 CC a disease associated with NF-kappaB activation, such as inflammation,
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
 CC neurodegenerative diseases, or ischaemic disorders.

XX
 SQ Sequence 438 AA;
 Query Match 96.5%; Score 436; DB 7; Length 438;
 Best Local Similarity 95.5%; Pred. No. 1.2e-47;
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVMYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60
 DB 203 KQORRELLFNEVIMRDYRHENVVMYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 262

QY 61 QIAAVCLAVLQALVLAHQGVTHSDIKTD 89
 DB 263 QIAAVCLAVLQALVLAHQGVTHSDIKTD 291

RESULT 8
 ADC37309
 ID ADC37309 standard; protein; 501 AA.

XX
 AC ADC37309;
 XX
 XX 18-DEC-2003 (first entry)

XX
 DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 142.
 XX
 KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
 KW cancer; infectious disease; bone disease; AIDS;
 KW neurodegenerative disease; ischaemic disorder; Antiinflammatory;
 KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
 KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human.

XX
 OS Homo sapiens.

PN WO2003048202-A2.
 XX
 PD 12-JUN-2003.
 XX
 PF 03-DEC-2002; 2002WO-JP012644.
 XX
 PR 03-DEC-2001; 2001JP-00368692.
 PR 05-DEC-2001; 2001US-0335829P.
 PR 03-OCT-2002; 2002JP-00291302.
 PR 04-OCT-2002; 2002US-0415769P.
 XX
 PA (ASAH) ASahi KASEI KK.
 XX
 PI Matsuda A, Muramatsu S;
 XX
 DR WPI; 2003-505282/47.
 DR N-PSDB; ADC37308.
 XX
 PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
 PT useful for treating inflammation, autoimmune diseases, cancers,
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
 PT ischemic disorders.
 XX
 PS Claim 1; SEQ ID NO 142; 938pp; English.
 XX
 CC The present invention relates to novel proteins and their coding
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
 CC kappaB). The proteins and their coding sequences are useful for treating
 CC a disease associated with NF-kappaB activation, such as inflammation,
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
 CC neurodegenerative diseases, or ischemic disorders.
 XX
 SQ Sequence 501 AA;
 Query Match 96.5%; Score 436; DB 7; Length 501;
 Best Local Similarity 95.5%; Pred. No. 1.4e-47;
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KQORRELLFNEVVIMRDYRHENNVEMNSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 60
 Db 266 KQORRELLFNEVVIMRDYQHENVNEMNSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 325
 QY 61 QIAAVCLAVLQALVLAHQGVTHSDIKTD 89
 Db 326 QIAAVCLAVLQALSVLAHQGVTHSDIKSD 354
 RESULT 9
 ID AAY55964
 XX AAY55964 standard; protein; 591 AA.
 AC AAY55964;
 XX
 DT 18-FEB-2000 (first entry)
 XX
 DE Full length human PAK5 protein.
 XX
 KW Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;
 KW antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;
 KW neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;
 KW vulnery; STE20; protein kinase; STLK3; STLK4; STLK5; STLK6; STLK7;
 KW ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GEK2; PAK4; PAK5; antagonist;
 KW antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
 KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
 KW rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
 KW myocardial infarction; cardiovascular disease; stroke; renal failure;
 KW oxidative stress-related neurodegenerative disorder; Parkinson's disease;
 KW amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
 KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
 KW mesangial disorder; growth regulation; wound healing; T cell activation;
 KW immunosuppressant.
 XX
 OS Homo sapiens.
 PN

XX WO9953036-A2.
 XX
 PD 21-OCT-1999.
 XX
 PF 13-APR-1999; 99WO-US008150.
 XX
 PR 14-APR-1998; 98US-0081784P.
 XX
 PA (SUGE-) SUGEN INC.
 XX
 PI Plowman G, Martinez R, Whyte D;
 XX
 DR WPI; 1999-611301/52.
 DR N-PSDB; AA240538.
 XX
 PT Novel kinase-related polypeptides used for the diagnosis and treatment of
 PT kinase-related diseases and disorders.
 XX
 PS Claim 11; Page 366-368; 387pp; English.
 XX
 CC This sequence represents a novel STE20-related protein kinase. The
 CC invention relates to nucleic acid molecule encoding a kinase polypeptide
 CC selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3,
 CC ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to
 CC identify agonists and antagonists, and to raise antibodies. The
 CC polynucleotides are useful in gene therapy protocols. The polynucleotides,
 CC polypeptides, antibodies, antagonists and agonists may be used to treat
 CC diseases such as immune-related disorders and diseases (e.g. rheumatoid
 CC arthritis, artherosclerosis, chronic inflammatory bowel disease (e.g.
 CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
 CC rhinitis, autoimmunity, and organ transplantation, chronic inflammatory
 CC pelvic disease, multiple sclerosis, organ transplantation, myocardial
 CC infarction, cardiovascular disease, stroke, renal failure, oxidative
 CC stress-related neurodegenerative disorders (e.g. amyotrophic lateral
 CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,
 CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
 CC mellitus, fibrotic and mesangial disorders. The proteins may also be
 CC useful for cell growth regulation (e.g. in wound healing), T cell
 CC activation, mitosis control, and as immunosuppressants
 XX
 SQ Sequence 591 AA;
 Query Match 96.5%; Score 436; DB 2; Length 591;
 Best Local Similarity 95.5%; Pred. No. 1.8e-47;
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KQORRELLFNEVVIMRDYRHENNVEMNSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 60
 Db 356 KQORRELLFNEVVIMRDYQHENVNEMNSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 415
 QY 61 QIAAVCLAVLQALVLAHQGVTHSDIKTD 89
 Db 416 QIAAVCLAVLQALSVLAHQGVTHSDIKSD 444
 RESULT 10
 ID AAY59128
 XX AAY59128 standard; protein; 591 AA.
 AC AAY59128;
 XX
 DT 08-MAR-2000 (first entry)
 XX
 DE Human serine/threonine kinase, PAK4.
 KW PAK4; serine/threonine kinase; GTPase; intracellular signal cascade; Rac;
 KW Cdc42H; morphogenesis; mitogenesis; JNK; p38 MAP kinase; human;
 KW actin polymerization; filopodia; cancer; arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO9963073-A1.

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XX 09-DEC-1999.
XX 21-MAY-1999; 99WO-US011341.
XX 21-MAY-1999; 98US-00082737.
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX Minden A;
XX WPI; 2000-072881/06.
XX N-PSDB; AA240657.
XX Novel mammalian nucleic acid useful for treating cancer and arthritis.
XX Claim 8; Fig 1A-B; 95pp; English.
XX The invention relates to an isolated mammalian nucleic acid that encodes
CC PAK4, a novel serine/threonine kinase or its mutant homolog. PAK4 is an
CC effector for the GTPases Rac and Cdc42Hs which are involved in
CC intracellular signal cascades, morphogenesis and mitogenesis, and
CC activate the JNK and p38 MAP kinase pathways. Inhibiting interaction of
CC PAK4 with these enzymes will thus result in inhibition of actin
CC polymerization and formation of filopodia. The PAK4 nucleic acid used for
CC recombinant production of the protein, and as a source of probes for
CC identifying homologous sequences and of (anti)sense oligonucleotides for
CC inhibiting PAK4 expression. The protein, or its fragments, are used to
CC raise specific antibodies and these are useful as ligands for therapeutic
CC inhibition of interaction between PAK4 and its native binding partners.
CC Inhibition of PAK4 activity or expression is used for treatment of cancer
CC and arthritis. The present sequence represents the human serine/threonine
CC kinase, PAK4
XX
XX Sequence 591 AA;
SQ
Query Match 96.5%; Score 436; DB 3; Length 591;
Best Local Similarity 95.5%; Pred. No. 1.8e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVEMVNSYLVGDELWVVMFELEGALTDIVTHRMNEE 60
Db 356 KQORRELLFNEVIMRDYQHENVVEMVNSYLVGDELWVVMFELEGALTDIVTHRMNEE 415

QY 61 QIAAVCLAVLQALVLAHQGVHSDIKTD 89
Db 416 QIAAVCLAVLQALSVLHAQGVHRIKSD 444

RESULT 11
ID ADC37307
XX ADC37307 standard; protein; 591 AA.
XX ADC37307;
XX 18-DEC-2003 (first entry)
XX Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 140.
XX Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
XX cancer; infectious disease; bone disease; AIDS;
XX neurodegenerative disease; ischaemic disorder; Antinflammatory;
XX Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
XX Neuroprotective; Nootropic; Cardiant; Gene therapy; human.
XX Homo sapiens.
XX WO2003048202-A2.
XX 12-JUN-2003.
XX 03-DEC-2002; 2002WO-JP012644.
XX

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PR 03-DEC-2001; 2001JP-00368692.
PR 05-DEC-2001; 2001US-0335829P.
PR 03-OCT-2002; 2002JP-00291302.
PR 04-OCT-2002; 2002US-0415769P.
XX (ASAH ) ASahi KASEI KK.
XX Matsuda A, Muramatsu S;
XX WPI; 2003-505282/47.
XX N-PSDB; ADC37306.
XX New purified protein that activates nuclear factor kappa B (NF-kappaB),
XX useful for treating inflammation, autoimmune diseases, cancers,
XX infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
XX ischemic disorders.
XX Claim 1; SEQ ID NO 140; 938pp; English.
XX The present invention relates to novel proteins and their coding
XX sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
XX kappaB). The proteins and their coding sequences are useful for treating
XX a disease associated with NF-kappaB activation, such as inflammation,
XX autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
XX neurodegenerative diseases, or ischaemic disorders.
XX Sequence 591 AA;
SQ
Query Match 96.5%; Score 436; DB 7; Length 591;
Best Local Similarity 95.5%; Pred. No. 1.8e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVEMVNSYLVGDELWVVMFELEGALTDIVTHRMNEE 60
Db 356 KQORRELLFNEVIMRDYQHENVVEMVNSYLVGDELWVVMFELEGALTDIVTHRMNEE 415

QY 61 QIAAVCLAVLQALVLAHQGVHSDIKTD 89
Db 416 QIAAVCLAVLQALSVLHAQGVHRIKSD 444

RESULT 12
ID ADD89973
XX ADD89973 standard; protein; 591 AA.
XX AC ADD89973;
XX 29-JAN-2004 (first entry)
XX Human cancer-associated protein kinase PAK4.
XX PAK4; protein kinase; enzyme; cancer; cytostatic; immunosuppressive;
XX antidiabetic; antirheumatic; antiarthritic; antipsoriatic;
XX angiogenic; antiarteriosclerotic; antiinflammatory; vulnerary;
XX gynaecological; neuroprotective; gene therapy; human.
XX Homo sapiens.
XX WO2003083096-A2.
XX 09-OCT-2003.
XX 21-MAR-2003; 2003WO-CA000409.
XX 28-MAR-2002; 2002US-0368853P.
XX (KINE-) KINETEK PHARM INC.
XX Delaney AD;
XX WPI; 2003-833542/77.
XX N-PSDB; ADD89972.
XX

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PI Mao Y, Xie Y, Gu Y;

```

DR WPI; 2001-489684/54.
DR N-PSDB; AAH44557.
XX
PT Human P21-active kinase 60 as one new kind of polypeptide and
XX polynucleotides encoding this polypeptide.
XX
PS Claim 1; Page 25-26 (Disclosure); 33pp; Chinese.
XX
CC The present sequence represents human P21-active kinase 60. The present
CC invention also describes a method of applying the polypeptide in treating
CC various diseases, such as malignant tumour, nosohemia, HIV infection,
CC immunological diseases and inflammations. Also described is an antagonist
CC resisting the polypeptide and its treatment effect
XX
SQ Sequence 547 AA;
Query Match 90.0%; Score 407; DB 4; Length 547;
Best Local Similarity 87.6%; Pred. No. 9.3e-44;
Matches 78; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60
DB 312 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 371
QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89
DB 372 QIATVCLSVLRALSYLHNQGVTHRDIKSD 400

RESULT 15
ID AAM38963 standard; protein; 719 AA.
XX
AC AAM38963;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2108.
XX
KW Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-0052317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSEQ-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
WPI; 2001-442253/47.
DR N-PSDB; AAI58119.
XX

```

Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

Example 3; SEQ ID NO 2108; 10078pp; English.

The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nontropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: immune system suppression, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification

Sequence 719 AA;

Query Match 90.0%; Score 407; DB 4; Length 719;
Best Local Similarity 87.6%; Pred. No. 1.4e-43;
Matches 78; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60
DB 484 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 543

QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89
DB 544 QIATVCLSVLRALSYLHNQGVTHRDIKSD 572

Search completed: September 29, 2004, 18:01:39
Job time : 24.2971 secs

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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:01:47 ; Search time 22.25 Seconds
(without alignments)
1287.197 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452

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Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	443	98.0	292	15	US-10-406-676-7
3	443	98.0	292	15	US-10-406-676-12
4	436	96.5	250	16	US-10-693-367-3
5	436	96.5	292	15	US-10-406-676-5
6	436	96.5	292	15	US-10-406-676-6
7	436	96.5	292	15	US-10-406-676-8
8	436	96.5	292	15	US-10-406-676-9
9	436	96.5	292	15	US-10-406-676-10
10	436	96.5	292	15	US-10-406-676-11
11	436	96.5	293	15	US-10-406-676-4
12	436	96.5	398	10	US-09-291-417-30
13	436	96.5	588	14	US-10-134-102-1
14	436	96.5	591	10	US-09-291-417-103
15	436	96.5	591	14	US-10-134-102-4

16	436	96.5	591	15	US-10-394-322A-48	Sequence 48, Appl
17	436	96.5	591	16	US-10-693-367-2	Sequence 2, Appl
18	421	93.1	292	15	US-10-406-676-15	Sequence 15, Appl
19	407	90.0	290	15	US-10-406-676-13	Sequence 13, Appl
20	407	90.0	719	14	US-10-331-095-2	Sequence 2, Appl
21	402	88.9	290	15	US-10-406-676-14	Sequence 14, Appl
22	402	88.9	290	15	US-10-406-676-16	Sequence 16, Appl
23	402	88.9	290	15	US-10-406-676-17	Sequence 17, Appl
24	402	88.9	580	15	US-10-108-260A-3288	Sequence 3288, Ap
25	402	88.9	719	14	US-10-331-095-4	Sequence 4, Appl
26	402	88.9	719	15	US-10-394-322A-49	Sequence 49, Appl
27	379	83.8	292	15	US-10-406-676-21	Sequence 21, Appl
28	379	83.8	641	16	US-10-311-034-15	Sequence 15, Appl
29	379	83.8	681	10	US-09-291-417-29	Sequence 29, Appl
30	376	83.2	681	10	US-09-765-815-2	Sequence 2, Appl
31	366	81.0	290	15	US-10-406-676-18	Sequence 18, Appl
32	366	81.0	290	15	US-10-406-676-19	Sequence 19, Appl
33	366	81.0	290	15	US-10-406-676-20	Sequence 20, Appl
34	366	81.0	635	14	US-10-134-102-2	Sequence 2, Appl
35	366	81.0	639	14	US-10-134-102-6	Sequence 6, Appl
36	303	67.0	540	15	US-10-369-493-6482	Sequence 6482, Ap
37	303	67.0	542	15	US-10-369-493-6483	Sequence 6483, Ap
38	283	62.6	704	12	US-10-267-502-378	Sequence 378, App
39	277	61.3	297	16	US-10-664-421-34	Sequence 34, Appl
40	277	61.3	305	10	US-09-765-815-10	Sequence 10, Appl
41	277	61.3	326	16	US-10-664-421-48	Sequence 48, Appl
42	277	61.3	545	9	US-09-967-624-5	Sequence 5, Appl
43	277	61.3	545	12	US-10-262-511-10	Sequence 30, Appl
44	277	61.3	545	12	US-10-267-502-380	Sequence 380, App
45	277	61.3	545	12	US-10-267-502-383	Sequence 383, App

ALIGNMENTS

RESULT 1

US-10-693-367-14
; Sequence 14, Application US/10693367
; Publication No. US20040091992A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
; FILE REFERENCE: 575/55311-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/693,367
; CURRENT FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: US/09/718,032
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11341
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/082,737
; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 89
; TYPE: PRT
; ORGANISM: mouse
; US-10-693-367-14

Query Match 100.0%; Score 452; DB 16; Length 89;
Best Local Similarity 100.0%; Pred. No. 7.9e-45;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	KQORRELLFNEVIMRDYRHENNVNYSYLVGDELWVMEFEGGALDIVVTHRMNEE	60
Db	1	KQORRELLFNEVIMRDYRHENNVNYSYLVGDELWVMEFEGGALDIVVTHRMNEE	60
Qy	61	QIAAVCLAVLQALAVLHAQGVHSDIKTD	89
Db	61	QIAAVCLAVLQALAVLHAQGVHSDIKTD	89

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RESULT 2
US-10-406-676-7
; Sequence 7, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 292
; TYPE: PRT
; ORGANISM: M.musculus
US-10-406-676-7

Query Match      98.0%; Score 443; DB 15; Length 292;
Best Local Similarity 97.8%; Pred. No. 3.8e-43;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVMNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60
Db 57 KQORRELLFNEVIMRDYRHENVVMNSYLVGDELWVMEFEGGALTDIVTHRMNEE 116

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
Db 117 QIAAVCLAVLQALAVLHAQGVHSDIKSD 145

RESULT 3
US-10-406-676-12
; Sequence 12, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 292
; TYPE: PRT
; ORGANISM: M.musculus
US-10-406-676-12

Query Match      98.0%; Score 443; DB 15; Length 292;
Best Local Similarity 97.8%; Pred. No. 3.8e-43;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVMNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60
Db 57 KQORRELLFNEVIMRDYRHENVVMNSYLVGDELWVMEFEGGALTDIVTHRMNEE 116

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
Db 117 QIAAVCLAVLQALAVLHAQGVHSDIKSD 145

RESULT 4
US-10-693-367-3
; Sequence 3, Application US/10693367
; Publication No. US20040091992A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
; FILE REFERENCE: 575/55311-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/693,367
; CURRENT FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: US/09/718,032
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11341
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/082,737
; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 250
; TYPE: PRT
; ORGANISM: human
US-10-693-367-3

Query Match      96.5%; Score 436; DB 16; Length 250;
Best Local Similarity 95.5%; Pred. No. 2e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVMNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60
Db 33 KQORRELLFNEVIMRDYQHENVVMNSYLVGDELWVMEFEGGALTDIVTHRMNEE 92

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
Db 93 QIAAVCLAVLQALSVLHAQGVHSDIKSD 121

RESULT 5
US-10-406-676-5
; Sequence 5, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5

Query Match      98.0%; Score 443; DB 15; Length 292;
Best Local Similarity 97.8%; Pred. No. 3.8e-43;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVMNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60
Db 57 KQORRELLFNEVIMRDYRHENVVMNSYLVGDELWVMEFEGGALTDIVTHRMNEE 116

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
Db 117 QIAAVCLAVLQALAVLHAQGVHSDIKSD 145

RESULT 5
US-10-406-676-5
; Sequence 5, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
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; Sequence 10, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H.sapiens
US-10-406-676-10

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.5e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVEMYNYSYLVGDELWVWMEFEGGALTDIVVTHTRMNEE 60
Db 57 KQORRELLFNEVIMRDYRHENVVEMYNYSYLVGDELWVWMEFEGGALTDIVVTHTRMNEE 116

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
Db 117 QIAAVCLAVLQALSVLHAQGVHSDIKSD 145

RESULT 11
US-10-406-676-4
; Sequence 4, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-676-4

Query Match          96.5%; Score 436; DB 15; Length 293;
Best Local Similarity 95.5%; Pred. No. 2.5e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVEMYNYSYLVGDELWVWMEFEGGALTDIVVTHTRMNEE 60
Db 58 KQORRELLFNEVIMRDYRHENVVEMYNYSYLVGDELWVWMEFEGGALTDIVVTHTRMNEE 117

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
Db 118 QIAAVCLAVLQALSVLHAQGVHSDIKSD 146

RESULT 12
US-09-291-417-30
; Sequence 30, Application US/09291417A
; Publication No. US20030050230A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 240/300
; CURRENT APPLICATION NUMBER: US/09/291,417A
; CURRENT FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: US 60/081,784
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Mammalian (Human) PAK5
US-09-291-417-30

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Query Match          96.5%; Score 436; DB 10; Length 398;
Best Local Similarity 95.5%; Pred. No. 3.6e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVVIMRDYQHENVNVMYNSYLVDLWVMEFEGGALTDIVTHTRMNEE 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 163 KQORRELLFNEVVIMRDYQHENVNVMYNSYLVDLWVMEFEGGALTDIVTHTRMNEE 222

QY 61 QIAAVCLAVLQALSVLHAQGVHSDIKTD 89
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 223 QIAAVCLAVLQALSVLHAQGVHSDIKTD 251

RESULT 13
US-10-134-102-1
; Sequence 1, Application US/10134102
; Publication No. US20030186254A1
; GENERAL INFORMATION:
; APPLICANT: Melnick, Michael B.
; APPLICANT: Moritz, Albrecht
; APPLICANT: Comb, Michael J.
; TITLE OF INVENTION: Regulation of HIV-Tat and Nef by the Pak4 kinase and its
; TITLE OF INVENTION: Binding partners and methods of identifying modulators thereof.
; FILE REFERENCE: CST-176 CIP
; CURRENT APPLICATION NUMBER: US/10/134,102
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 09/750,457
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/173,939
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-134-102-1

Query Match          96.5%; Score 436; DB 14; Length 588;
Best Local Similarity 95.5%; Pred. No. 5.8e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVVIMRDYQHENVNVMYNSYLVDLWVMEFEGGALTDIVTHTRMNEE 60
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Db 356 KQORRELLFNEVVIMRDYQHENVNVMYNSYLVDLWVMEFEGGALTDIVTHTRMNEE 415

QY 61 QIAAVCLAVLQALSVLHAQGVHSDIKTD 89
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 416 QIAAVCLAVLQALSVLHAQGVHSDIKTD 444

RESULT 14
US-09-291-417-103
; Sequence 103, Application US/09291417A
; Publication No. US20030050230A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 240/300
; CURRENT APPLICATION NUMBER: US/09/291,417A
; CURRENT FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: US 60/081,784
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 103
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Full Length Mammalian (Human) PAK5hu
US-09-291-417-103
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Query Match          96.5%; Score 436; DB 10; Length 591;
Best Local Similarity 95.5%; Pred. No. 5.9e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVVIMRDYQHENVNVMYNSYLVDLWVMEFEGGALTDIVTHTRMNEE 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 356 KQORRELLFNEVVIMRDYQHENVNVMYNSYLVDLWVMEFEGGALTDIVTHTRMNEE 415

QY 61 QIAAVCLAVLQALSVLHAQGVHSDIKTD 89
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 416 QIAAVCLAVLQALSVLHAQGVHSDIKTD 444

RESULT 15
US-10-134-102-4
; Sequence 4, Application US/10134102
; Publication No. US20030186254A1
; GENERAL INFORMATION:
; APPLICANT: Melnick, Michael B.
; APPLICANT: Moritz, Albrecht
; APPLICANT: Comb, Michael J.
; TITLE OF INVENTION: Regulation of HIV-Tat and Nef by the Pak4 kinase and its
; TITLE OF INVENTION: Binding partners and methods of identifying modulators thereof.
; FILE REFERENCE: CST-176 CIP
; CURRENT APPLICATION NUMBER: US/10/134,102
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 09/750,457
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/173,939
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-134-102-4

Query Match          96.5%; Score 436; DB 14; Length 591;
Best Local Similarity 95.5%; Pred. No. 5.9e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVVIMRDYQHENVNVMYNSYLVDLWVMEFEGGALTDIVTHTRMNEE 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 356 KQORRELLFNEVVIMRDYQHENVNVMYNSYLVDLWVMEFEGGALTDIVTHTRMNEE 415

QY 61 QIAAVCLAVLQALSVLHAQGVHSDIKTD 89
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 416 QIAAVCLAVLQALSVLHAQGVHSDIKTD 444

Search completed: September 29, 2004, 18:09:25
Job time : 22.25 secs
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OM protein - protein search, using sw model

Run on: September 29, 2004, 17:58:42 ; Search time 6.15147 Seconds
(without alignments)
746.929 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452

Sequence: 1 KQORRELFNEVIMRDYRH.....LQALAVLHAQGVTHSDIKTD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/prodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	452	100.0	89	US-09-718-032-14	Sequence 14, Appl
2	436	96.5	250	US-09-082-737-3	Sequence 3, Appl
3	436	96.5	250	US-09-718-032-3	Sequence 3, Appl
4	436	96.5	398	US-09-688-188B-30	Sequence 30, Appl
5	436	96.5	398	US-09-291-417D-30	Sequence 30, Appl
6	436	96.5	591	US-09-082-737-2	Sequence 2, Appl
7	436	96.5	591	US-09-688-188B-103	Sequence 103, App
8	436	96.5	591	US-09-718-032-2	Sequence 2, Appl
9	436	96.5	591	US-09-291-417D-103	Sequence 103, App
10	379	83.8	681	US-09-688-188B-29	Sequence 29, Appl
11	379	83.8	681	US-09-291-417D-29	Sequence 29, Appl
12	376	83.2	681	US-09-765-815-2	Sequence 2, Appl
13	277	61.3	244	US-09-163-507-2	Sequence 2, Appl
14	277	61.3	268	US-08-852-743-3	Sequence 3, Appl
15	277	61.3	268	US-09-185-370-3	Sequence 3, Appl
16	277	61.3	305	US-09-765-815-10	Sequence 10, Appl
17	277	61.3	465	US-08-114-555A-2	Sequence 2, Appl
18	277	61.3	465	US-08-559-397A-2	Sequence 2, Appl
19	276	61.1	245	US-09-163-507-3	Sequence 3, Appl
20	276	61.1	545	US-08-935-760-4	Sequence 4, Appl
21	276	61.1	545	US-09-688-188B-93	Sequence 93, Appl
22	276	61.1	545	US-09-291-417D-93	Sequence 93, Appl
23	274	60.6	244	US-09-163-507-1	Sequence 1, Appl
24	274	60.6	524	US-08-615-942A-2	Sequence 2, Appl
25	274	60.6	524	US-09-237-325-2	Sequence 2, Appl
26	274	60.6	544	US-08-935-760-2	Sequence 2, Appl
27	274	60.6	544	US-08-559-397A-19	Sequence 19, Appl

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28      269      59.5      544      4      US-09-688-188B-95      Sequence 95, Appl
29      269      59.5      544      4      US-09-291-417D-95      Sequence 95, Appl
30      288      59.3      544      3      US-08-559-397A-30      Sequence 30, Appl
31      286      58.8      250      4      US-09-718-032-4      Sequence 4, Appl
32      266      58.8      506      1      US-08-369-780-2      Sequence 2, Appl
33      266      58.8      506      1      US-08-475-682-2      Sequence 2, Appl
34      266      58.8      506      1      US-08-780-833-2      Sequence 2, Appl
35      266      58.8      506      1      US-08-636-036-2      Sequence 2, Appl
36      266      58.8      506      3      US-08-918-509-2      Sequence 2, Appl
37      286      58.8      506      3      US-09-108-262-2      Sequence 2, Appl
38      266      58.8      506      4      US-09-688-188B-94      Sequence 94, Appl
39      266      58.8      506      4      US-09-291-417D-94      Sequence 94, Appl
40      255      56.4      250      4      US-09-718-032-5      Sequence 5, Appl
41      255      56.4      251      3      US-09-082-737-5      Sequence 5, Appl
42      255      56.4      271      2      US-08-852-743-4      Sequence 4, Appl
43      255      56.4      271      3      US-09-185-370-4      Sequence 4, Appl
44      255      56.4      694      3      US-08-559-397A-31      Sequence 31, Appl
45      249      55.1      544      3      US-08-559-397A-29      Sequence 29, Appl

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ALIGNMENTS

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RESULT 1
US-09-718-032-14
; Sequence 14, Application US/09718032
; Patent No. 6667168
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
; FILE REFERENCE: 575/55311-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/718,032
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11341
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/082,737
; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 89
; TYPE: PRT
; ORGANISM: mouse
US-09-718-032-14

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Query Match      100.0%; Score 452; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.6e-50;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1      KQORRELFNEVIMRDYRHENVMYNSYLVGDELWVMEFEGGALTDIVTHTRMNEE 60
Db      1      KQORRELFNEVIMRDYRHENVMYNSYLVGDELWVMEFEGGALTDIVTHTRMNEE 60

QY      61      QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
Db      61      QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89

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RESULT 2
US-09-082-737-3
; Sequence 3, Application US/09082737
; Patent No. 6013500
; GENERAL INFORMATION:
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4; A No. 6013500e1 Gene Encoding A Serine/
; TITLE OF INVENTION: Threonine Kinase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York

```

	Query Match	96.5%	Score 436;	DB 4;	Length 250;
	Best Local Similarity	95.5%	Pred. No. 7.6e-48;		
	Matches 85;	Conservative 3;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	KQQRRELLFNEVIMRDYQHENVVMYNSYLVGDDELVVMVEFLGGALTDIVTHRMNEE	60		
Db	33	KQQRRELLFNEVIMRDYQHENVVMYNSYLVGDDELVVMVEFLGGALTDIVTHRMNEE	92		
Qy	61	QIAAVCLAVLQALAVIHAQGVITHDIKTD	89		

Query Match	96.5%	Score 436;	DB 4;	Length 398;
Best Local Similarity	95.5%;	Pred. No.	1.4e-47;	
Matches	85;	Conservative	3;	Mismatches 1; Indels 0; Gaps 0;
Qy	1	KQQRRELLFNEVIMRDYRHENVVEMYSNLVGDELWVMVEFLGGALTDIVHTRMNEE	60	
Dd	163	KQQRRELLFNEVIMRDYQHENVVEMYSNLVGDELWVMVEFLGGALTDIVHTRMNEE	222	
Qy	61	QIAAVCLAVLQAALVAHLHAQGVIHSDIKTD	89	
Dd	223	QIAAVCLAVLQAALSVLHAQGVIHRDKSD	251	

RESULT 6
US-09-082-737-2
; Sequence 2, Application US/09082737
; Patent No. 6013500
; GENERAL INFORMATION:
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4; A No. 6013500el Gene Encoding A Serine/
; TITLE OF INVENTION: Threonine Kinase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1195 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11230
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,737
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/55311
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NOS: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-082-737-2

Query Match 96.5%; Score 436; DB 3; Length 591;
Best Local Similarity 95.5%; Pred. No. 2.5e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVVMRDYRHENNVNMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 60
Db 356 KQORRELLFNEVVMRDYRHENNVNMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 415

QY 61 QIAAVCLAVLQALSVLHAQGVHSDIKTD 89
Db 416 QIAAVCLAVLQALSVLHAQGVHSDIKTD 444

RESULT 7
US-09-688-188B-103
; Sequence 103, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 103
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-103

Query Match 96.5%; Score 436; DB 4; Length 591;
Best Local Similarity 95.5%; Pred. No. 2.5e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVVMRDYRHENNVNMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 60
Db 356 KQORRELLFNEVVMRDYRHENNVNMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 415

QY 61 QIAAVCLAVLQALSVLHAQGVHSDIKTD 89
Db 416 QIAAVCLAVLQALSVLHAQGVHSDIKTD 444

RESULT 8
US-09-718-032-2
; Sequence 2, Application US/09718032
; Patent No. 6667168
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4; A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
; FILE REFERENCE: 575/55311-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/718,032
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11341
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/082,737
; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 591
; TYPE: PRT
; ORGANISM: human
US-09-718-032-2

Query Match 96.5%; Score 436; DB 4; Length 591;
Best Local Similarity 95.5%; Pred. No. 2.5e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVVMRDYRHENNVNMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 60
Db 356 KQORRELLFNEVVMRDYRHENNVNMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 415

QY 61 QIAAVCLAVLQALSVLHAQGVHSDIKTD 89
Db 416 QIAAVCLAVLQALSVLHAQGVHSDIKTD 444

RESULT 9
US-09-291-417D-103
; Sequence 103, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 103
; LENGTH: 591

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-103

Query Match      96.5%; Score 436; DB 4; Length 591;
Best Local Similarity 95.5%; Pred. No. 2.5e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQQRRELLFNEVIMRDYRHENNVVYNSYLVGDELWVVMFELEGALTDIVVTHRMNEE 60
   |||||
Db 356 KQQRRELLFNEVIMRDYQHFNVVMYKSYLVGDELWVVMFELEGALTDIVVTHRMNEE 415
   |||||

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
   |||||
Db 416 QIAAVCLAVLQALAVLHAQGVHSDIKTD 444

RESULT 10
US-09-688-188B-29
; Sequence 29, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-29

Query Match      83.8%; Score 379; DB 4; Length 681;
Best Local Similarity 83.1%; Pred. No. 5.9e-40;
Matches 74; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KQQRRELLFNEVIMRDYRHENNVVYNSYLVGDELWVVMFELEGALTDIVVTHRMNEE 60
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Db 442 KQQRRELLFNEVIMRDYQHFNVVMYKSYLVGDELWVVMFELEGALTDIVVTHRMNEE 501
   |||||

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
   |||||
Db 502 QIATVCEAVLQALAVLHAQGVHSDIKTD 530

RESULT 11
US-09-291-417D-29
; Sequence 29, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-29

Query Match      83.8%; Score 379; DB 4; Length 681;
Best Local Similarity 83.1%; Pred. No. 5.9e-40;
Matches 74; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KQQRRELLFNEVIMRDYRHENNVVYNSYLVGDELWVVMFELEGALTDIVVTHRMNEE 60
   |||||
Db 442 KQQRRELLFNEVIMRDYQHFNVVMYKSYLVGDELWVVMFELEGALTDIVVTHRMNEE 501
   |||||

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
   |||||
Db 502 QIATVCEAVLQALAVLHAQGVHSDIKTD 530

RESULT 12
US-09-765-815-2
; Sequence 2, Application US/09765815
; Patent No. 6673586
; GENERAL INFORMATION:
; APPLICANT: Balk, Steven
; TITLE OF INVENTION: No. 6673586el Steroid Hormone Receptor
; TITLE OF INVENTION: Interacting Protein Kinase
; FILE REFERENCE: 01948/068002
; CURRENT APPLICATION NUMBER: US/09/765,815
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/176,859
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-765-815-2

Query Match      83.2%; Score 376; DB 4; Length 681;
Best Local Similarity 82.0%; Pred. No. 1.4e-39;
Matches 73; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 KQQRRELLFNEVIMRDYRHENNVVYNSYLVGDELWVVMFELEGALTDIVVTHRMNEE 60
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Db 442 KQQRRELLFNEVIMRDYQHFNVVMYKSYLVGDELWVVMFELEGALTDIVVTHRMNEE 501
   |||||

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
   |||||
Db 502 QIATVCEAVLQALAVLHAQGVHSDIKTD 530

RESULT 13
US-09-163-507-2
; Sequence 2, Application US/09163507
; Patent No. 6383734
; GENERAL INFORMATION:
; APPLICANT: Marshall, M. S.
; APPLICANT: Diaz, H. B.
; APPLICANT: King, A. J.
; APPLICANT: Sun, H.
; TITLE OF INVENTION: Method to determine inhibition of RAF3
; FILE REFERENCE: 740.001US1
; CURRENT APPLICATION NUMBER: US/09/163,507
; CURRENT FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-163-507-2

Query Match      61.3%; Score 277; DB 4; Length 244;

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Blank

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 17:38:51 ; Search time 2.48676 Seconds
(without alignments)
1863.563 Million cell updates/sec

Title: US-10-693-367-14
Perfect score: 452
Sequence: 1 KQORRELLFNEVVIMEDYRH.....LQALAVLHAQGVHSDIKTD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	436	96.5	591	PAK4 HUMAN	O96013 homo sapien
2	402	88.9	719	PAK7 HUMAN	O9p286 homo sapien
3	379	83.8	681	PAK6 HUMAN	O9nqu5 homo sapien
4	277	61.3	544	PAK1 RAT	P35465 rattus norv
5	277	61.3	545	PAK1 HUMAN	O13153 homo sapien
6	277	61.3	545	PAK1 MOUSE	O88643 mus musculu
7	276	61.1	544	PAK3 HUMAN	O75914 homo sapien
8	276	61.1	544	PAK3 RAT	O62829 rattus norv
9	274	60.6	524	PAK2 HUMAN	O13177 homo sapien
10	274	60.6	524	PAK2 RABIT	O29502 oryctolagus
11	274	60.6	524	PAK2 RAT	O64303 rattus norv
12	269	59.5	544	PAK3 MOUSE	O61036 mus musculu
13	256	56.6	1230	ST20 CANAL	O92212 candida alb
14	255	56.4	939	ST20 YEAST	O03497 saccharomyc
15	248.5	55.0	971	CLA4 CANAL	O14427 candida alb
16	231.5	51.2	842	CLA4 YEAST	P48562 saccharomyc
17	231	51.1	658	PAK1 SCHPO	P50527 schizosacch
18	220.5	48.8	589	SHK2 SCHPO	O10056 schizosacch
19	203.5	45.0	855	SKM1 YEAST	O12469 saccharomyc
20	180.5	39.9	821	M4K2 MOUSE	O61161 mus musculu
21	177.5	39.3	819	M4K2 HUMAN	O12851 h mitogen-a
22	172.5	38.2	681	M4K3 MOUSE	O991p0 mus musculu
23	172.5	38.2	862	M4K3 RAT	O92412 rattus norv
24	172.5	38.2	894	M4K3 HUMAN	O8i9v8 homo sapien
25	170.5	37.7	833	M4K1 HUMAN	O92918 homo sapien
26	170.5	37.7	847	M4K5 MOUSE	O8bpm2 mus musculu
27	169.5	37.5	846	M4K5 HUMAN	O9y4k4 homo sapien
28	164.5	36.4	827	M4K1 MOUSE	P70218 mus musculu
29	161	35.6	1308	M4K6 MOUSE	O9jms2 mus musculu
30	161	35.6	1332	M4K6 HUMAN	O8n4c8 homo sapien
31	157.5	34.8	547	SPAK HUMAN	O9uew8 homo sapien
32	157.5	34.8	553	SPAK RAT	O88506 rattus norv
33	157.5	34.8	556	SPAK_MOUSE	O9z1w9 mus musculu

34	157	34.7	916	1	TNIK MOUSE	P83510 mus musculu
35	157	34.7	1360	1	TNIK_HUMAN	O9uRe5 homo sapien
36	151.5	33.5	1401	1	WIS4 SCHPO	O14299 schizosacch
37	151	33.4	944	1	NER9_XENLA	O7zzc8 xenopus lae
38	148.5	32.9	652	1	NAK1 SCHPO	O75011 schizosacch
39	146	32.3	1233	1	M4K1 MOUSE	P97820 mus musculu
40	145.5	32.2	1080	1	M115_CAEEL	O23356 caenorhabdi
41	145.5	32.2	1314	1	SS22_YEAST	P25390 saccharomyc
42	145	32.1	471	1	SIDI SCHPO	O14305 schizosacch
43	145	32.1	1239	1	M4K4 HUMAN	O95819 homo sapien
44	141.5	31.3	1050	1	ULK1_HUMAN	O75385 homo sapien
45	141.5	31.3	1051	1	ULK1_MOUSE	O70405 mus musculu

ALIGNMENTS

RESULT 1
PAK4_HUMAN
ID_PAK4_HUMAN STANDARD; PRT; 591 AA.
AC O96013; Q9BU33;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase PAK 4 (EC 2.7.1.-) (p21-activated
kinase 4) (PAK-4).
GN PAK4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=99043860; PubMed=9822598;
RA Abo A., Qu J., Cammarano M.S., Dan C., Fritsch A., Baud V.,
Bellisle B., Minden A.;
RT "PAK4, a novel effector for Cdc42Hs, is implicated in the
reorganization of the actin cytoskeleton and in the formation of
filopodia";
RT EMBO J. 17:6527-6540(1998).
RN [2]
RX SEQUENCE FROM N.A. (ISOFORM 1).
RA MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Strausberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richard S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Hellon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smallos D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: ACTIVATES THE JNK PATHWAY. IMPLICATED IN THE
REORGANIZATION OF THE ACTIN CYTOSKELETON AND IN THE FORMATION OF
FILOPODIA.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH RAC1.
CC CDC42/P21 AND WEAKLY WITH RAC1.


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CC      -!- SIMILARITY: Contains 1 CRIB domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AB040812; BAA94194.1; --
DR      EMBL; AB033090; BAA86578.1; ALT INIT.
DR      EMBL; AL353612; CAC34367.1; --
DR      HSP; P24941; 1BUH.
DR      Genew; HGNC:15916; PAK7.
DR      MIM; 608038; --
DR      InterPro; IPR000095; PAKbox/RhoBndng.
DR      InterPro; IPR000719; Prot Kinase.
DR      InterPro; IPR008271; Ser thr pkin AS.
DR      InterPro; IPR002290; Ser thr pkinase.
DR      InterPro; IPR001245; Tyr_pkinase.
DR      Pfam; PF00786; PBD; 1.
DR      Pfam; PF00069; pkinase; 1.
DR      PRINTS; PR00109; TYRKINASE.
DR      ProDom; PD000001; Prot Kinase; 1.
DR      SMART; SM00285; PBD; 1.
DR      SMART; SM00220; S_TKC; 1.
DR      PROSITE; PS50108; CRIB; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE NEG.
KW      Transferase; Serine/threonine-protein kinase; ATP-binding;
KW      Phosphorylation.
FT      DOMAIN 11 24 CRIB.
FT      DOMAIN 25 448 LINKER.
FT      DOMAIN 449 700 PROTEIN KINASE.
FT      NP_BIND 455 463 ATP (BY SIMILARITY).
FT      BINDING 478 478 ATP (BY SIMILARITY).
FT      ACT_SITE 568 568 BY SIMILARITY.
SQ      SEQUENCE 719 AA; 80744 MW; 07A12BEEC4E2A02 CRC64;

Query Match      88.9%; Score 402; DB 1; Length 719;
Best Local Similarity 86.5%; Pred. No. 1.1e-33;
Matches 77; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY      1 KOORRELLFNEVIMRDYHENVVYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60
DB      484 KOORRELLFNEVIMRDYHENVVYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 543
QY      61 QIAAVCLAVLQALVLAHQGVHSDIKTD 89
DB      544 QIATVCLSVLRALSYLVNQGVIHRDIKSD 572

RESULT 3
ID      PAK6 HUMAN
AC      Q9NQ05;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Serine/threonine-protein kinase PAK 6 (EC 2.7.1.-) (p21-activated
DE      kinase 6) (PAK-6) (PAK-5).
GN      PAK6 OR PAK5.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21226785; PubMed=11278661;
RA      Yang F., Li X., Sharma M., Zarnegar M., Lim B., Sun Z.;
RT      "Androgen receptor specifically interacts with a novel p21-activated

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RT      kinase, PAK6.";
RN      J. Biol. Chem. 276:15345-15353(2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Wagner T., Puls A., Frischauf A.M., Hall A.;
RT      "PAK5, a new member of the p21-activated kinase family, affects Cdc42
RT      signalling to the actin cytoskeleton.";
RL      Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA      Whitling M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA      Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length
RT      human and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC      -!- FUNCTION: The activated kinase acts on a variety of targets (By
CC      similarity).
CC      -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC      CDC42/P21 AND RAC1 (BY SIMILARITY). INTERACTS WITH THE ANDROGEN
CC      RECEPTOR.
CC      -!- PTM: Autophosphorylated when activated by CDC42/p21 (By
CC      similarity).
CC      -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC      STE20 subfamily.
CC      -!- SIMILARITY: Contains 1 CRIB domain.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF276893; AAF82800.1; --
DR      EMBL; AJ236915; AAC18720.1; --
DR      EMBL; BC035596; AAB35596.1; --
DR      Genew; HGNC:16061; PAK6.
DR      MIM; 608110; --
DR      HSP; P24941; 1A01.
DR      InterPro; IPR000095; PAKbox/RhoBndng.
DR      InterPro; IPR000719; Prot Kinase.
DR      InterPro; IPR008271; Ser thr pkin AS.
DR      InterPro; IPR002290; Ser thr pkinase.
DR      InterPro; IPR001245; Tyr_pkinase.
DR      Pfam; PF00786; PBD; 1.
DR      Pfam; PF00069; pkinase; 1.
DR      PRINTS; PR00109; TYRKINASE.
DR      ProDom; PD000001; Prot Kinase; 1.
DR      SMART; SM00285; PBD; 1.
DR      SMART; SM00220; S_TKC; 1.
DR      PROSITE; PS50108; CRIB; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE NEG.
KW      Transferase; Serine/threonine-protein kinase; ATP-binding;

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KW Phosphorylation.
FT DOMAIN 12 25 CRIB.
FT DOMAIN 26 406 LINKER.
FT DOMAIN 407 658 PROTEIN KINASE.
FT NP_BIND 413 421 ATP (BY SIMILARITY).
FT BINDING 436 436 ATP (BY SIMILARITY).
FT ACT_SITE 526 526 ATP (BY SIMILARITY).
SQ SEQUENCE 681 AA; 74868 MW; F20A4FA257649BB9 CRC64;

Query Match 83.8%; Score 379; DB 1; Length 681;
Best Local Similarity 83.1%; Pred. No. 2.5e-31;
Matches 74; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 KQORRELFNEVIMRDYRHENVMYNSYLVDGLWVMEFLGGALTDIVTHTRMNEE 60
Db 442 KQORRELFNEVIMRDYRHENVMYNSYLVDGLWVMEFLGGALTDIVTHTRMNEE 501

Qy 61 QIAAVCLAVLQALVLAHQGVHSDIKTD 89
Db 502 QIATVCEAVLQALVLAHQGVHSDIKTD 530

RESULT 4
PAK1_RAT
ID PAK1_RAT STANDARD; PRT; 544 AA.
AC P35465; Q62934;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-) (p21-activated
DE kinase 1) (PAK-1) (P65-PAK) (Alpha-PAK) (Protein kinase MUK2).
GN PAK1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP Nature 367:40-46(1994).
RC TISSUE=Brain;
RX MEDLINE=94150588; PubMed=8107774;
RA Manser E., Leung T., Salihuddin H., Zhao Z.-S., Lim L.;
RA "A brain serine/threonine protein kinase activated by Cdc42 and
RT Rac1.";
RL Nature 367:40-46(1994).
RN [2]
RP REVISIONS.
RA Zhao Z.-S.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Osada S.-I., Izawa M., Saito R., Mizuno K., Suzuki A., Hirai S.-I.,
RA Ohno S.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=96027610; PubMed=7559638;
RA Lim L.;
RA "Molecular cloning of a new member of the p21-Cdc42/Rac-activated
RT kinase (PAK) family.";
RL J. Biol. Chem. 270:25070-25078(1995).
CC -!- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.
CC LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED
CC GTPASES TO THE JNK MAP KINASE PATHWAY.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/p21 AND RAC1 (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE BRAIN, WITH
CC HIGHER EXPRESSION IN NEURONAL GROUPS ASSOCIATED WITH MOTOR
CC FUNCTION, AND AT LOWER LEVELS IN THE SPLEEN.
CC -!- DEVELOPMENTAL STAGE: FOUND IN THE EMBRYONIC CNS WITH LITTLE
CC EXPRESSION ELSEWHERE.
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
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CC STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC -----
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CC -----
CC EMBL; U23443; AAB95646.1; -.
CC EMBL; U49953; AAB61533.1; -.
CC PDB; 1E0A; 14-SEP-00.
CC InterPro; IPR000095; PAKbox/RhoGndng.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_kin_AS.
CC InterPro; IPR002290; Ser_thr_kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC Pfam; PF00786; PBD; 1.
CC Pfam; PF00069; pkinase; 1.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00285; PBD; 1.
CC SMART; SM00220; S_TRK; 1.
CC PROSITE; PS00108; CRIB; 1.
CC PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; 3D-structure.
FT DOMAIN 75 88 CRIB.
FT DOMAIN 89 268 LINKER.
FT DOMAIN 269 520 PROTEIN KINASE.
FT NP_BIND 275 283 ATP (BY SIMILARITY).
FT BINDING 298 298 ATP (BY SIMILARITY).
FT ACT_SITE 388 388 BY SIMILARITY.
SQ SEQUENCE 544 AA; 60577 MW; 93BE32D822F5B7B CRC64;

Query Match 61.3%; Score 277; DB 1; Length 544;
Best Local Similarity 58.4%; Pred. No. 5.5e-21;
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

Qy 1 KQORRELFNEVIMRDYRHENVMYNSYLVDGLWVMEFLGGALTDIVTHTRMNEE 60
Db 304 QQPKELIINEILVMRENKPNVNYLDSYLVGDELWVMEYLAGSLTDVVTETCMDEG 363

Qy 61 QIAAVCLAVLQALVLAHQGVHSDIKTD 89
Db 364 QIAAVCRECLQALFLHNSQVHTRDIKSD 392

RESULT 5
PAK1_HUMAN
ID PAK1_HUMAN STANDARD; PRT; 545 AA.
AC Q13153; Q13567;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase PAK 1 (EC 2.7.1.37) (p21-activated
DE kinase 1) (PAK-1) (P65-PAK) (Alpha-PAK).
GN PAK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97199447; PubMed=9395435;
RA Sells M.A., Knaus U.G., Bagrodia S., Ambrose D.M., Bokoch G.M.,
RA Chernoff J.;
RT "Human p21-activated kinase (Pak1) regulates actin organization in
RT mammalian cells.";
```

RL Curr. Biol. 7:202-210(1997).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=96398842; PubMed=8805275;
 RA Brown J.L., Stowers L., Baer M., Trejo J., Coughlin S., Chant J.;
 RT "Human Ste20 homologue hPAK1 links GTPases to the JNK MAP kinase
 RT pathway.";
 RL Curr. Biol. 6:598-605(1996).
 RN [3]
 RN FUNCTION, AND INTERACTION WITH CDC2L1 AND CDC2L2.
 RX MEDLINE=22651041; PubMed=12624090;
 RA Chen S., Yin X., Zhu X., Yan J., Ji S., Chen C., Cai M., Zhang S.,
 RA Zong H., Hu Y., Yuan Z., Shen Z., Gu J.;
 RT "The C-terminal kinase domain of the p34cdc2-related PITSURE protein
 RT kinase (p110C) associates with p21-activated kinase 1 and inhibits
 RT its activity during anokis.";
 RL J. Biol. Chem. 278:20029-20036(2003).
 CC -!- FUNCTION: The activated kinase acts on a variety of targets.
 CC Likely to be the GTPase effector that links the Rho-related
 CC GTPases to the JNK MAP kinase pathway. Activity inhibited in cells
 CC undergoing apoptosis, potentially due to binding of CDC2L1 and
 CC CDC2L2.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- COFACTOR: Magnesium.
 CC -!- SUBUNIT: Interacts tightly with GTP-bound but not GDP-bound
 CC CDC42/p21 and RAC1. Binds to the caspase-cleaved p110 isoform of
 CC CDC2L1 and CDC2L2, p110C, but not the full-length proteins.
 CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
 CC STE20 subfamily.
 CC -!- SIMILARITY: Contains 1 CRIB domain.
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 CC
 CC EMBL; U24152; AAA65441.1; -;
 CC EMBL; U51120; AAC50590.1; -;
 CC PIR; G01773; G01773.
 CC PDB; 1E3M; 29-NOV-00.
 CC Genew; HGNC:8590; PAK1.
 CC MIM; 602590; -;
 CC GO; GO:0007254; P:JNK cascade; TAS.
 CC GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
 CC InterPro; IPR000095; PAKbox/RhoBndng.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR008271; Ser_thr_pkin_AS.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC Pfam; PF00786; PBD; 1.
 CC Pfam; PF00069; pkinase; 1.
 CC PRINTS; PR00109; TYRKINASE.
 CC PRODom; PD000001; Prot_kinase; 1.
 CC SMART; SM00285; PBD; 1.
 CC SMART; SM00220; S_TK; 1.
 CC PROSITE; PS0108; CRIB; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Apoptosis; Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation; 3D-structure.
 FT DOMAIN 75 88 CRIB.
 FT 89 269 LINKER.
 FT DOMAIN 270 521 PROTEIN_KINASE.
 FT NP_BIND 276 284 ATP (BY SIMILARITY).
 FT BINDING 299 299 ATP (BY SIMILARITY).
 FT ACT_SITE 389 389 BY SIMILARITY.
 FT MUTAGEN 107 107 L->F: CONSTITUTIVELY ACTIVE.

FT CONFLICT 26 26 V -> A (IN REF. 2).
 FT CONFLICT 237 237 R -> L (IN REF. 2).
 FT CONFLICT 379 379 F -> S (IN REF. 2).
 FT CONFLICT 503 503 D -> E (IN REF. 2).
 SQ SEQUENCE 545 AA; 60661 MW; 14A1E70B6480CD7E CRC64;
 Query Match 61.3%; Score 277; DB 1; Length 545;
 Best Local Similarity 58.4%; Pred No. 5.6e-21;
 Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;
 QY 1 KQORELLFNEVIMRDYRHENVVMYNSYLVGDELWVMEFEGGALFDIVYTHRMNSE 60
 Db 305 QQPKKELINEILVMKKNPNIVLDSYLVGDELWVMEYLAGSLTDVVVTCMDRG 364
 QY 61 QTAACVLAQLQALVLAHQGVTHSDIKTD 89
 Db 365 QTAACVRECLQALEFLHSNQVHRIKSD 393
 RESULT 6
 PAK1 MOUSE
 ID PAK1 MOUSE STANDARD; PRT; 545 AA.
 AC O88643;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-) (p21-activated
 DE kinase 1) (PAK-1) (p65-PAK) (Alpha-PAK) (CDC42/RAC effector kinase
 DE PAK-A).
 GN PAK1 OR PAKA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99282526; PubMed=10352232;
 RA Burchelo P.D., Korak C.A., Finegold A.A., Hall A., Pirone D.M.;
 RT "Cloning, central nervous system expression and chromosomal mapping of
 RT the mouse PAK-1 and PAK-3 genes.";
 RL Gene 232:209-215(1999).
 CC -!- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.
 CC LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED
 CC GTPASES TO THE JNK MAP KINASE PATHWAY (BY SIMILARITY).
 CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
 CC CDC42/p21 AND RAC1 (BY SIMILARITY).
 CC -!- PTM: Autophosphorylated when activated by CDC42/p21 (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
 CC STE20 subfamily.
 CC -!- SIMILARITY: Contains 1 CRIB domain.
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 CC
 CC EMBL; AF082077; AAC32375.1; -;
 CC HSSP; P24941; 1CKP.
 CC MGD; MGI:133975; Pak1.
 CC GO; GO:0005737; Cytoplasm; IDA.
 CC GO; GO:0016358; P:dendrite morphogenesis; IDA.
 CC InterPro; IPR000095; PAKbox/RhoBndng.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR008271; Ser_thr_pkin_AS.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC Pfam; PF00786; PBD; 1.
 CC Pfam; PF00069; pkinase; 1.
 CC PRINTS; PR00109; TYRKINASE.

```
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0285; PBD; 1.
DR SMART; SMO0220; S TKC; 1.
DR PROSITE; PS00108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 75 88 CRIB
FT DOMAIN 89 267 LINKER.
FT DOMAIN 270 521 PROTEIN KINASE.
FT NP_BIND 276 284 ATP (BY SIMILARITY).
FT BINDING 299 299 ATP (BY SIMILARITY).
FT ACT_SITE 389 389 BY SIMILARITY.
SQ SEQUENCE 545 AA; 60737 MW; A4861289534C3819 CRC64;

Query Match 61.3%; Score 277; DB 1; Length 545;
Best Local Similarity 58.4%; Pred. No. 5.6e-21;
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHNENVMNSYLVGDELWVMEFLEGALTDIVTHRMNEE 60
DB 305 QQPKKELLINEILVMRENKNFNIVNLYDSYLVGDELWVMEYLAGGSLTDVVTETCMDEG 364

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 365 QIAAVCRECLQALEFLHNSQVTHRIDKSD 393

RESULT 7
PAK3 HUMAN
ID PAK3 HUMAN STANDARD; PRT; 544 AA.
AC Q75914;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase PAK 3 (EC 2.7.1.1-) (p21-activated
DE kinase 3) (PAK-3) (Beta-PAK) (Oligophrenin-3).
GN PAK3 OR OPHN3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND DISEASE.
RX MEDLINE=98400251; PubMed=9731525;
RA Allen K.M., Gleeson J.G., Bagrodia S., Partington M.W.,
RA Macmillan J.C., Cerione R.A., Mulley J.C., Walsh C.A.;
RT "PAK3 mutation in nonsyndromic X-linked mental retardation.";
RL Nat. Genet. 20:25-30(1998).
CC -!- FUNCTION: The activated kinase acts on a variety of targets.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3
CC DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN POSTMITOTIC NEURONS OF THE
CC DEVELOPING AND POSTNATAL CEREBRAL CORTEX AND HIPPOCAMPUS.
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- DISEASE: Defects in PAK3 are the cause of non-specific X-linked
CC nonsyndromic mental retardation type 30 (MRX30) [MIM:300142].
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC ST20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC -----
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CC -----
CC EMBL; AF068864; AAC36097.1; --
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DR HSSP; P24941; ICKP.
DR Genew; HGNC:8592; PAK3.
DR MIM; 300142; -.
DR InterPro; IPR000095; PAKbox/RhoBindng.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0285; PBD; 1.
DR SMART; SMO0220; S TKC; 1.
DR PROSITE; PS00108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW SH3-binding; Phosphorylation.
FT DOMAIN 70 83 CRIB.
FT DOMAIN 84 267 LINKER.
FT DOMAIN 268 519 PROTEIN KINASE.
FT NP_BIND 274 282 ATP (BY SIMILARITY).
FT BINDING 297 297 ATP (BY SIMILARITY).
FT ACT_SITE 387 387 BY SIMILARITY.
SQ SEQUENCE 544 AA; 60692 MW; 230AF6952CB049E2 CRC64;

Query Match 61.1%; Score 276; DB 1; Length 544;
Best Local Similarity 58.4%; Pred. No. 7e-21;
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHNENVMNSYLVGDELWVMEFLEGALTDIVTHRMNEE 60
DB 303 QQPKKELLINEILVMRENKNFNIVNLYDSYLVGDELWVMEYLAGGSLTDVVTETCMDEG 362

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 363 QIAAVCRECLQALDPLHNSQVTHRIDKSD 391

RESULT 8
PAK3 RAT
ID PAK3 RAT STANDARD; PRT; 544 AA.
AC Q62829;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase PAK 3 (EC 2.7.1.1-) (p21-activated
DE kinase 3) (PAK-3) (Beta-PAK) (P65-PAK).
GN PAK3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE OF 37-56.
RX MEDLINE=96027610; PubMed=7559638;
RA Manser E., Chong C., Zhao Z.-S., Leung T., Michael G., Hall C.,
RA Lim L.;
RT "Molecular cloning of a new member of the p21-Cdc42/Rac-activated
RT kinase (PAK) family.";
RL J. Biol. Chem. 270:25070-25078(1995).
CC -!- FUNCTION: The activated kinase acts on a variety of targets.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3
CC DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK (BY
CC SIMILARITY).
CC -!- TISSUE SPECIFICITY: DETECTED AT HIGH LEVELS IN THE BRAIN AND AT
CC LOW LEVELS IN THE TESTIS.
CC -!- DEVELOPMENTAL STAGE: FOUND IN THE EMBRYONIC CNS WITH LITTLE
CC EXPRESSION ELSEWHERE.
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FT CONFLICT 90 A -> T (IN REF. 2).
FT CONFLICT 150 L -> F (IN REF. 2).
FT CONFLICT 225 P -> T (IN REF. 2).
FT CONFLICT 329 G -> R (IN REF. 2).
FT CONFLICT 338 T -> TA (IN REF. 1).
SQ SEQUENCE 524 AA; 58004 MW; DE2A7A72BE6B1072 CRC64;

Query Match 60.6%; Score 274; DB 1; Length 524;
Best Local Similarity 58.4%; Pred. No. 1.1e-20;
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYLVGDELWVMEFLEGGALTDIVVTHRMNEE 60
Db 284 KQPKKELIINEILVMKELKNPNVNFVLDYLVGDELWVMEYLAGGLSDVVTETCMDEA 343

QY 61 QIAAVCLAVLOALVILHAQGVHSDIKTD 89
Db 344 QIAAVCRECLQALEFLHANQVHRIKSD 372

RESULT 10
ID_PAK2 RABIT STANDARD; PRT; 524 AA.
AC Q29502;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase PAK 2 (EC 2.7.1.-) (p21-activated
DE kinase 2) (PAK-2) (Gamma-PAK) (p21-activated protein kinase 1)
DE (PAK1).
DE PAK2.
GN Oryctolagus cuniculus (Rabbit).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198078; PubMed=8626411;
RA Jakobi R., Chen C., Tuazon P.T., Traugh J.A.;
RT "Molecular cloning and sequencing of the cytosolic G protein-
RT activated protein kinase PAK 1."
RL J. Biol. Chem. 271:6206-6211(1996).
CC -!- FUNCTION: The activated kinase acts on a variety of targets.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/p21 AND RAC1.
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U46915; AAC48537.1; -.
CC HSP; P24941; LKXP.
CC InterPro; IPR000095; PAKbox/RhoGndng.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF00786; PBD; 1.
CC Pfam; PF00069; pkinase; 1.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00285; PBD; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS0108; CRIB; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
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DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 74 87 CRIB.
FT DOMAIN 88 248 LINKER.
FT DOMAIN 249 500 PROTEIN_KINASE.
FT NP_BIND 255 263 ATP (BY SIMILARITY).
FT BINDING 278 278 ATP (BY SIMILARITY).
FT ACT_SITE 368 368 BY SIMILARITY.
SQ SEQUENCE 524 AA; 58027 MW; 39D71020EADFFCA CRC64;

Query Match 60.6%; Score 274; DB 1; Length 524;
Best Local Similarity 58.4%; Pred. No. 1.1e-20;
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYLVGDELWVMEFLEGGALTDIVVTHRMNEE 60
Db 284 KQPKKELIINEILVMKELKNPNVNFVLDYLVGDELWVMEYLAGGLSDVVTETCMDEA 343

QY 61 QIAAVCLAVLOALVILHAQGVHSDIKTD 89
Db 344 QIAAVCRECLQALEFLHANQVHRIKSD 372

RESULT 11
ID_PAK2 RAT STANDARD; PRT; 524 AA.
AC Q64303;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase PAK 2 (EC 2.7.1.-) (p21-activated
DE kinase 2) (PAK-2) (Gamma-PAK) (P62-PAK).
DE PAK2.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=Brain, and Testis;
RX MEDLINE=96064759; PubMed=7592896;
RA Teo M., Manser E., Lim L.;
RT "Identification and molecular cloning of a p21cdc42/rac1-activated
RT serine/threonine kinase that is rapidly activated by thrombin in
RT platelets".
RL J. Biol. Chem. 270:26690-26697(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Mabel T.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: The activated kinase acts on a variety of targets.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/p21 AND RAC1.
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S80221; AAB35608.1; -.
CC EMBL; U35345; AAA79064.1; -.
CC HSP; P24941; LKXP.
CC InterPro; IPR000095; PAKbox/RhoGndng.
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DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 74 87 CRIB.
FT DOMAIN 88 248 LINKER.
FT DOMAIN 249 500 PROTEIN_KINASE.
FT NP_BIND 255 263 ATP (BY SIMILARITY).
FT BINDING 278 278 ATP (BY SIMILARITY).
FT ACT_SITE 368 368 BY SIMILARITY.
SQ SEQUENCE 524 AA; 57960 MW; A3F2FE81C8D4294 CRC64;

Query Match 60.6%; Score 274; DB 1; Length 524;
Best Local Similarity 58.4%; Pred. No. 1.1e-20;
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYRHENVMYNSYLVDGLWVMEFLGGLTIDVTHTRMNEE 60
DB 284 KOPKXELINEILVMKELKNPNIYFLSYLVDGLWVMEFLGGLTIDVTHTRMNEE 60
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
DB 344 QIAAVCRECLQALFLHNSQVHHRDIKSD 372

RESULT 12
PAK3 MOUSE
ID_PAK3_MOUSE STANDARD; PRT; 544 AA.
AC Q61036; O88645;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-) (p21-activated
DE kinase 3) (PAK-3) (Beta-PAK) (CDC42/RAC effector kinase PAK-B).
GN PAK3 OR PAK-3 OR STK4 OR PAKB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
(1) SEQUENCE FROM N.A.
RC TISSUE=Fibroblast;
RX MEDLINE=96032893; PubMed=7559398;
RA Bagrodia S., Taylor S.J., Creasy C.L., Chernoff J., Cerione R.A.;
RT "Identification of a mouse p21cdc42/Rac activated kinase.";
RL J. Biol. Chem. 270:22731-22737(1995).
RN [2]
RP ERRATUM.
RA Bagrodia S., Taylor S.J., Creasy C.L., Chernoff J., Cerione R.A.;
RL J. Biol. Chem. 271:1250-1250(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99282526; PubMed=10352232;
RA Burdello P.D., Kozak C.A., Finesold A.A., Hall A., Pirone D.M.;
RT "Cloning, central nervous system expression and chromosomal mapping of
RT the mouse PAK-1 and PAK-3 genes.";
RL Gene 232:209-215(1999).
CC -!- FUNCTION: The activated kinase acts on a variety of targets.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3
CC DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK.

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CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; U39738; AAC52354.1; -
CC EMBL; AF082297; AAC31969.1; -
CC PIR; I49376; I49376.
CC PDB; 1BES; 12-APR-00.
CC MGD; MGI:1339656; Pak3.
CC InterPro; IPR000095; PAKbox/RhoGndng.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF00786; PBD; 1.
CC Pfam; PF00069; pkinase; 1.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00285; PBD; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS00108; CRIB; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW SH3-binding; Phosphorylation; 3D-structure.
FT DOMAIN 70 83 CRIB.
FT DOMAIN 84 267 LINKER.
FT DOMAIN 268 519 PROTEIN_KINASE.
FT NP_BIND 274 282 ATP (BY SIMILARITY).
FT BINDING 297 297 ATP (BY SIMILARITY).
FT ACT_SITE 387 387 BY SIMILARITY.
FT CONFLICT 161 161 G -> A (IN REF. 3).
FT CONFLICT 361 361 V -> E (IN REF. 3).
FT CONFLICT 493 493 H -> R (IN REF. 3).
FT CONFLICT 525 525 L -> M (IN REF. 3).
SQ SEQUENCE 544 AA; 60693 MW; C4AEB7D33B6988 CRC64;

Query Match 59.5%; Score 269; DB 1; Length 544;
Best Local Similarity 57.3%; Pred. No. 3.7e-20;
Matches 51; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYRHENVMYNSYLVDGLWVMEFLGGLTIDVTHTRMNEE 60
DB 303 QOPKXELINEILVMKELKNPNIYFLSYLVDGLWVMEFLGGLTIDVTHTRMNEE 60
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
DB 363 QIAAVCRECLQALFLHNSQVHHRDIKSD 391

RESULT 13
ST20 CANAL
ID_ST20_CANAL STANDARD; PRT; 1230 AA.
AC Q92212;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase STE20 homolog (EC 2.7.1.-).
GN HST20 OR GST20.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;

```

```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=1066;
RX  MEDLINE=97075146; PubMed=8917572;
RA  Kohler J.R., Fink G.R.;
RT  "Candida albicans strains heterozygous and homozygous for mutations
RT  in mitogen-activated protein kinase signaling components have defects
RT  in hyphal development.";
RL  Proc. Natl. Acad. Sci. U.S.A. 93:13223-13228(1996).
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC  -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC  STE20 subfamily.
CC  -!- SIMILARITY: Contains 1 CRIB domain.
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CC  or send an email to license@isb-sib.ch).
CC  EMBL; U73457; AAB38875.1; -.
DR  PIR; T18259; T18259.
DR  HSSP; Q63450; 1A06.
DR  InterPro; IPR000095; PAKbox/RhoGndng.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR008271; Ser_thr_pkin_AS.
DR  InterPro; IPR002290; Ser_thr_pkinase.
DR  InterPro; IPR001245; Tyr_pkinase.
DR  Pfam; PF00786; PKB; 1.
DR  Pfam; PF00069; pkinase; 1.
DR  PRINTS; PR00109; TYRKINASE.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  SMART; SM00285; PKB; 1.
DR  SMART; SM00220; S_TK; 1.
DR  PROSITE; PS0108; CRIB; 1.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW  Transferase; Serine/threonine-protein kinase; ATP-binding.
FT  DOMAIN 109 119 POLY-ASN.
FT  DOMAIN 290 293 POLY-PRO.
FT  DOMAIN 453 464 POLY-SER.
FT  DOMAIN 552 555 POLY-SER.
FT  DOMAIN 573 580 POLY-GLY.
FT  DOMAIN 727 732 POLY-PRO.
FT  DOMAIN 790 794 POLY-PRO.
FT  DOMAIN 475 488 CRIB.
FT  DOMAIN 953 1205 PROTEIN_KINASE.
FT  NP_BIND 959 967 ATP (By similarity).
FT  BINDING 983 983 ATP (By similarity).
FT  ACT_SITE 1073 1073 BY SIMILARITY.
SQ  SEQUENCE 1230 AA; 132862 MW; 2B2AC4C133B9FE81 CRC64;

Query Match          56.6%; Score 256; DB 1; Length 1230;
Best Local Similarity 50.6%; Pred. No. 1.8e-18;
Matches 45; Conservative 21; Mismatches 23; Indels 0; Gaps 0;

QY  1 KQORRELFNEVIVRDYHENVEMNSYLVGDELWVMEFEGGALTDIVTHTRMEE 60
DB  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  989 QQPKKELINEILVMKGSHPNINVIDSYLLKGLDWIMETMEGSLTDIVTHSVMTG 1048
QY  61 QIAAVCLAVLOALVLHAGVTHSDIKTD 89
DB  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  1049 QIGVVCRETLLKGLKFLHSGVHHRDIKSD 1077

RESULT 14
ST20 YEAST
ID ST20_YEAST STANDARD; PRT; 939 AA.
AC Q03497;
DT 01-OCT-1993 (Rel. 27, Created)
```

01-OCT-1993 (Rel. 27, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serine/threonine-protein kinase STE20 (EC 2.7.1.-).
STE20 OR YHL007C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NCBI_TaxID=4932;
[1]
SEQUENCE FROM N.A.
MEDLINE=93099855; PubMed=1464311;
Leberer E., Dignard D., Harscus D., Thomas D.Y., Whiteway M.;
"The protein kinase homolog Ste20p is required to link the yeast
pheromone response G-protein beta gamma subunits to downstream
signalling components";
EMBO J. 11:4815-4824(1992).
[2]
SEQUENCE FROM N.A.
MEDLINE=93133807; PubMed=8421676;
Ramer S.W., Davis R.W.;
"A dominant truncation allele identifies a gene, STE20, that encodes
a putative protein kinase necessary for mating in Saccharomyces
cerevisiae";
Proc. Natl. Acad. Sci. U.S.A. 90:452-456(1993).
[3]
SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
MEDLINE=94378003; PubMed=8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hallier L.W., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,
Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
Vaudin M.;
"Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
VIII";
Science 265:2077-2082(1994).
CC -!- FUNCTION: Required to link the pheromone response G-protein beta
gamma subunits to downstream signaling components. It is thought
that it can phosphorylate STE5. Needed for mating in haploid
cells, induction of a mating-specific gene FUS1, induction of
mating-specific morphologies, and pheromone-induced proliferation
arrest. Phosphorylates STE11.
CC -!- PATHWAY: Response to pheromone-induced signal.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: Autophosphorylated on serine residues.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
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CC EMBL; M94719; AAA35111.1; -.
CC EMBL; L04655; AAA35038.1; -.
CC EMBL; L04655; AAA35039.1; -.
CC EMBL; U11581; AAB69747.1; -.
CC PIR; S28394; S28394.
CC HSSP; Q63450; 1A06.
CC GenOnline; 139274; -.
CC SGD; S0000999; STE20.
CC GO; GO:0000131; C:incipient bud site; IDA.
CC GO; GO:0005937; C:shmoo tip; IDA.
CC GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
CC GO; GO:0000282; P:bud site selection; IMP.
CC GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
CC InterPro; IPR000095; PAKbox/RhoGndng.

```

DR InterPro; IPR000719; Prot Kinase.
DR InterPro; IPR008271; Ser Thr pkin AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot Kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Pheromone response; Phosphorylation.
FT DOMAIN 337 350 CRIB.
FT DOMAIN 620 871 PROTEIN KINASE.
FT NP BIND 626 634 ATP (BY SIMILARITY).
FT BINDING 649 649 ATP (BY SIMILARITY).
FT ACT SITE 739 739 BY SIMILARITY.
FT CONFLICT 19 19 N -> S (IN REF. 2).
FT CONFLICT 134 134 I -> M (IN REF. 2).
FT CONFLICT 271 271 P -> S (IN REF. 2).
SQ SEQUENCE 939 AA; 102362 MW; 69C1C12F5B87733C CRC64;

Query Match 56.4%; Score 255; DB 1; Length 939;
Best Local Similarity 48.3%; Pred. No. 1.8e-18;
Matches 43; Conservative 23; Mismatches 23; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVEMNSYLVGDELWVVMFLEGALTDIVTHRMNE 60
DB 655 KQPKELIINEILVWKGSKHNVFNFDISVYLVKGLWIMVMEGSLTDVVTCHILTEG 714

QY 61 QIAAVCLAVLQALVLAHAGVHSDIKTD 89
DB 715 QIGAVCRETLGLEFLHSGKGLVLRDIKSD 743

RESULT 15
CLA4 CANAL STANDARD; PRT; 971 AA.
AC O14427;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase CLA4 (EC 2.7.1.-).
GN CLA4.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97411146; PubMed=9259554;
RA Leberer E., Ziegelbauer K., Schmidt A., Marcus D., Dignard D., Ash J.,
RA Johnson L., Thomas D.Y.
RT "Virulence and hyphal formation of Candida albicans require the
RT Ste20p-like protein kinase CaCl4p."
RL Curr. Biol. 7:539-546(1997).
RC -!- FUNCTION: Essential for virulence and morphological switching
RC (hyphal formation) of C.albicans.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC -----
DR EMBL; U87996; AAB68613.1; -.
DR HSSP; Q63450; IA06.
DR InterPro; IPR000095; PAKbox/RhoBindng.
DR InterPro; IPR001849; PH.
DR PRINTS; PR00109; Prot Kinase.
DR InterPro; IPR008271; Prot Thr pkin AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot Kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS0003; PH DOMAIN; 1.
DR PROSITE; PS0107; PROTEIN KINASE ATP; FALSE_NEG.
DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 67 178 PH.
FT DOMAIN 231 244 CRIB.
FT DOMAIN 680 935 PROTEIN KINASE.
FT DOMAIN 16 19 POLY-PRO.
FT DOMAIN 210 213 POLY-SER.
FT DOMAIN 311 315 POLY-ASN.
FT DOMAIN 384 389 POLY-ASN.
FT DOMAIN 392 395 POLY-ASN.
FT DOMAIN 418 421 POLY-PRO.
FT DOMAIN 453 462 POLY-GLN.
FT DOMAIN 468 476 POLY-GLN.
FT DOMAIN 572 576 POLY-GLN.
FT NP BIND 686 694 ATP (BY SIMILARITY).
FT BINDING 710 710 ATP (BY SIMILARITY).
FT ACT SITE 803 803 BY SIMILARITY.
SQ SEQUENCE 971 AA; 106889 MW; AD6F0DBBC6CF624B CRC64;

Query Match 55.0%; Score 248.5; DB 1; Length 971;
Best Local Similarity 47.3%; Pred. No. 8.5e-18;
Matches 43; Conservative 27; Mismatches 18; Indels 3; Gaps 2;

QY 2 QORRELLFNEVIMRDYRHENVVEMNSYLVGDELWVVMFLEGALTDIVTHRT--RMN 58
DB 717 QPKELIINEILVWKGSKHNVFNFDISVYLVKGLWIMVMEGSLTEIENNDFKLN 776

QY 59 EEQIAAVCLAVLQALVLAHAGVHSDIKTD 89
DB 777 EKQIATICFETLKGLOLHUKKHIHRDIKSD 807

Search completed: September 29, 2004, 18:02:01
Job time : 2.48676 secs

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